

TITLE Cloning and sequencing of cDNA encoding bovine tumor necrosis factor (TNF)-receptor I
 JOURNAL Vet. Immunol. Immunopathol. 61 (2-4), 379-385 (1998)
 MEDLINE 98273505
 PUBMED 9613449
 REFERENCE 2 (bases 1 to 2440)
 AUTHORS Lee, B.-K., Talyor, M.J. and Kehrli, M.E.
 TITLE Direct Submission
 JOURNAL Submitted (26-PEB-1997) Metabolic Disease and Immunology, National Animal Disease Center, 2300 Dayton Ave., Ames, IA 50010, USA

FEATURES
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BASE COUNT 441 a 771 c 701 g 527 t
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Query Match 100.0%; Score 2440; DB 4; Length 2440;
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SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 2004)
AUTHORS     Suter,B. and Pauli,U.
TITLE       Cloning of the CDNA encoding the porcine p55 tumor necrosis factor
            receptor
JOURNAL     Gene 163
MEDLINE     96011645
PubMed     7590278
REFERENCE   2 (bases 1 to 2004)
AUTHORS     Pauli,U.H.
TITLE       Direct Submission
JOURNAL     Submitted (19-JAN-1995) Urs H. Pauli, Veterinary Virology,
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 VERSION
 AB051103.1
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 REFERENCE
 AUTHORS
 Mizuno, T., Goto, Y., Baba, K., Masuda, K., Ohno, K. and Tezujimoto, H.
 TITLE
 TNF-alpha-induced cell death in feline immunodeficiency
 virus-infected cells is mediated by the caspase cascade
 JOURNAL
 Virology 287 (2), 446-455 (2001)
 MEDLINE
 21425403
 PUBMED
 11531421
 2 (bases 1 to 2171)
 REFERENCE
 AUTHORS
 Mizuno, T.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (14-NOV-2000) Takuya Mizuno, The University of Tokyo,
 Department of Veterinary Internal Medicine, Yayoi 1-1-1, Bunkyo-ku,
 Tokyo 113-8657, Japan [E-mail: a47715@mail.ecc.u-tokyo.ac.jp,
 Tel: 81-3-5841-8004, Fax: 81-3-5841-8178]
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COMMENT
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: mgc-help@nci.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nci.nih.gov
Shenker, Y., Wechter, K.D., Beckstrom-Sternberg, S.M.,
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Lim, M., Maduro, O.L., Mastaglio, S.D., McCluskey, J.C.,
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Tongson, E.E., Touchman, J.W., Tsougen, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IPAL Plate: 27 Row: n Column: 22
This clone was selected for full length sequencing because it
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OY	421	CCTGTCCCAAGGAATATATACCAACCCGGAATATGACCATTTGCTGCACCAAGTGC	480
Db	368	TGTGTCCCAAGGAATATATACCAACCCGGAATATGACCATTTGCTGCACCAAGTGC	427
OY	481	ACAAAGGTACTATCTGACAAATGACTGTCCGGGTCCAGGGGAGACAGGATCGAGGG	540
Db	428	ACAAAGGAACCTTACTGTACATGACTGTCCAGCCCGGGGACAGGATACGAACTGAGGG	487
OY	541	TGTGTGCCCCCTGGCACCTACACTGCTTGGAGAACCATTCAGACGATGCTGAGTGTCT	600
Db	488	ACTGTGAGAGCCGGCTCTTCCACCGCTTCAGAAACCACTCAGACACTGCTCAGTGTCT	547
OY	601	CCAGGTCGCGGGACGAATGTTCCAGGTGGAGATTTGGCTTGTGTATGTGACCCGGACA	660
Db	548	CCAAATGCCGAAGGAATGGGTCAAGTGGAAATCTCTTTCGACAGTGGACCCGGACA	607
OY	661	CTGTGTGCGGCTGCGAGGAAGAACAGATACCGGGAATACTGGGGTGAACATGGCTTCCGGT	720
Db	608	CGTGTGTGGCTGCGAGGAAGAACAGATACCGGCAATATTGGAGTGAACCTTTCCAGT	667
OY	721	GTCTGAACGTGAGGCTCTGTCCCAATGGCAGCATGATATCCCTGCGCAGAGAGACAGG	780
Db	668	GCTTCAATTTGACGCTCTGTCCCTCAATGGGACCGTGCACCTCTCTCCCGAGGAACAGA	727
OY	781	ACACCATCTGCCACATGATATGAGCTTCTTTCTTAAAGGCCACAGTGCATCTCTGTG	840
Db	728	ACACCGTGTGACCTGTGCCATGCAAGTTCTTTCTTAAAGGAACCAAGTGTGTCTCTGTA	787
OY	841	ATGATTTGTAAAGAA---CAAGAGTGGAGAGTTATGTTCAAACCGACCTTCAACTGTGTA	897
Db	788	GTAACCTGTAAAGAAAGCCGTGAGTGCACGAAAGTTGTGCTTACCCAGATTGGAATGTTA	847
OY	898	AAGATCTCAGGAGCCAGGACATACAGTACTATTAACCCCTGGTGAATGTCTTCCGGGCTTT	957
Db	848	AGGGACATGAGGACCTCAGGACACCAAGTGTCTTGTCCCTGTGTCAATTTCTTGTGTCTT	907
OY	958	GCTTGGCATCTTTCGCTCTGTGTCTTGTAGCATGTGTCTTCCAGCGGTGGAAGCCCAAGC	1017
Db	908	GCTTTTATCTCTCTCTTCTTCAATTTGATTAAATGTATGTGCTTACCAAGGTGGAAATGCAGC	967
OY	1018	TCTACTCATCATTTTGGGGGACGTGACCTGTGTAAAGAGGGGAGGCCAAGAA-----	1070
Db	968	TCTACTCATATGTTTGTGGGAATGCAACCTGTAAAGAGGGGAGGCTTAAAGAACTTA	1027
OY	1071	--CTCTGGTCCCGGCCCCAGGCTTCAACCCCAACCAACCATCTGTTCAGCTTCAACC	1128
Db	1028	CTACTTAACCCCTGTGGCCCCCAAAACCAAGCTTCAGTCCCACTCCAGCTTCAACCCCAACC	1087
OY	1129	CAAGTTCAGTCTGTCTTTCATCTCCCTTATATCTCTGTGACCGGTTCACATTTCGGAG	1188
Db	1088	TGGGCTTCAAGTCCCTGTGCCAGTTCACATCTTCACTTCAGGTTCACCTATATACCCCGGTG	1147
OY	1189	-----CCGTGCAATCTCTCTCAGAGAGACGGGCCCGCCCATCTTAAAGGTGTGGC	1239
Db	1148	ACTGTCCCAACTTTGTGGGCTCCCGGCAAGAGGTGGACACACCTATCAGAGGGGCTTACC	1207
OY	1240	CCATTCCTCCCGGGGCTCCGGGCTTCACCACTCTGTATACCCCGGGGCTTCGGCTTCA	1299
Db	1208	CCATTCCT-----	1214
OY	1300	CCCACTCTGTACCCCGGGGCTCGGGCTGCACACCATCTGTGACCCCAATTCAGAACT	1359
Db	1215	-----TGGCAACAGCTCTGCTCTGACCCCATCCCAACCCCTTCAAGAACT	1261

QY	1360	GGGAAGCAGGAGCCCCCAGGGCCCCCGATACAGCTCGGGAAATGGCCAGCCCCGACCTCT	1413
Db	1262	GGGAGACAGCGCCACAC--AGCCACAGAGCCTTAGACACTGATGACCCCGGACGCTGT	1318
QY	1420	ACGCGGTGTGGACGCGCGTGCCTCCCGCTGCCTGTGAAGAGATTGGTCCGCGCGCTGGGAC	1479
Db	1319	ACGCGGTGTGTGAAGACGTGCCTCCCGCTGTGCCTGTGAAGAAATTCTTCGCGGCTTAGGGC	1378
QY	1480	TGAGCGAGCACGACATGACGCGGCTGGAGCTGTGAAGACGGGCGCCACCTGCGCGAGCGC	1539
Db	1379	TGACCGACACAGAAATCGATGCGCTGGAGCTGCAAGACGGGCGCTGCCTGCGCGAGCGC	1438
QY	1540	AGTACAGCATGCTTGGCGGCGCTGGCGGGCGGCGGACACCGCGCCCGGAGAGCCACCTTGAGAC	1599
Db	1439	AATACAGATGCTTGGCGACCTGGAGGGCGGCGGACACCGCGCGCGAGGCCACGCTTGAGC	1498
QY	1600	TGCTTGGCGCGGCTGCTCAGGAGACATTGACCTGCTGGGTTGGCTTGGAAAACATAGAGAGG	1659
Db	1499	TGCTTGGGACCGGTCTCTCGGACATTTGACCTGCTGGGCTGCTTGGAGAGACATTCAGGAGG	1558
QY	1660	CGCTTGGGTGGCGCGCGCCGCTTGCGATTCGAGGCCCGCCTTCTCTGTGAAGCCCCCGCC	1719
Db	1559	CGCTTGGCGGCGCGCGCCCTCCCGCGCGCGCCAGCTTTCTTCAGATGAGGCTGCGCC	1618
QY	1720	CTCCG 1724	
Db	1619	CTGGG 1623	

RESULT 6	
HUMTNFRC	
LOCUS	2112 bp mRNA linear PRI 03-AUG-1993
DEFINITION	Human tumor necrosis factor receptor (TNF receptor) mRNA, complete cds.
ACCESSION	M61121 M75861
VERSION	M61121.1 GI:339755
KEYWORDS	tumor necrosis factor receptor.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 2112) Hummel,A., Maurer-Fogy,I., Kronke,M., Scheurich,P., Pfeizemer,K., Lantuz,M., Olsson,I., Hauptmann,R., Sratowa,C. and Adolf,G.R.
TITLE	Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p50) and its soluble derivative, tumor necrosis factor-binding protein
JOURNAL	DNA Cell Biol. 9 (10), 705-715 (1990)
MEDLINE	91090841
PUBMED	1702293
COMMENT	Original
FEATURES	source text: Human cDNA to mRNA. location/Olaaffiers
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CDS	207..1574
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sig_peptide 207..293
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mat_peptide 294..1571
/gene="TNF receptor"
/product="tumor necrosis factor receptor"

BASE COUNT 435 a 632 c 589 g 456 t
ORIGIN

Query Match 30.24; Score 735.8; DB 9; Length 2112;
Best Local Similarity 69.94; Pred. No. 8.9e-119;
Matches 1152; Conservative 0; Mismatches 402; Indels 95; Gaps 8;

101 GGGCGGAGGCTGGGCTTCCGGGTTGAGCTCCCGATGGGCTGNG---TCCCGCC 157
11 GGGCTCAGATTGCGCTTTGGGGTTCAAGATCATCGGACCAAGCCGATCTATGCC 70
158 CAGCTTCACCCCTCCACTCCCGACCCGAGGCCGGGCTCCACTGGGCAATACGAGGA 217
71 CAGCTTCACCCCTCCACTCCCGACCCGAGGCCGATCGCTCCGAGACAGACGAGTC 130
218 CCGTGTCTCTCACTGTCGGGGCCGCACTGCCCC-AGCCCTGATNGGGGATTGAGAG 276
131 CCGGAGAGCCCGACACTGCGCTGCGACACTGCTGAGCCCAATGAGGAGTGAAG 190
277 GCGACAGTGGCCGAGCATGGGCTCCCGACGTCGCTGCTGCTGCACTGATGTC 336
191 GCGATAGTGTCTGG-CATGGGCTCTCCACCGTCCGACCTGCTGCTGCACTGATGC 249
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250 TCCTGAGACTGTGGTGGAAATATATACCCCTCAGGGGTTATTGAGCTGTCCCTCACCTAG 309
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637 GCGCTTGTGTAGTGAACCGGAGACATGTGTGGGCTGAGAGAAACAGTACCGGGAAT 696
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670 ACCTTCTTCGACGAGAGAGAGACACATCTGTCACCTGCAATATGGCTTCTTTCTTA 729
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730 GAGAGAGAGAGTGTGTCTCTTGTATGATGTAAGTGAAGAGCCGAGAGTSCAGAGATTC 789
874 GTCCAAACCCGACCTTCACTGTAAGACTCTCAGAGCCGAGGCACTACAGTACTATTC 933
790 GCGTACCCGAGATGTAAGTGAAGGAGCTGAGAGACTCAGGCACTACAGTGTGCTTGC 849
934 CCGTGTGTATGATCTTGGGCTTGTGCTGAGCACTCCCTGCTGTGCTGCTTATGAGATGC 993
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910 GCTACCAAGGTGAGAGTCCAACTTACTTCACTTGTGTTGTGAGAAATCCACACTGAA 969
1054 AAGAGGGAGAGCCAGAA-----CTCGTGTCCCGGCGCCAGAGTTCAACCCCA 1104
970 AAGAGGGAGAGCTTGAAGAACTATCTAAGAGCCCTGCGCCCAACCCAGCTTCACTC 1029
1105 CCACATCTGCTTCACTGCTCAACCCCAAGTTCAGTCTCTGCTTCATTCCTCCCTTACATCT 1164
1030 CCACTCAGAGCTTCAACCCCAAGTTCAGTCTCTGCTTCAGTCTCTGCTTCACCTTCACT 1089
1165 CCGTGTGACCGGTTCACCTTGAAG-----CCGTGCACTCTCTCTTCAAGCAGAGCG 1215
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1441 CCGGCGCGGAGGACCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 1500
1636 GTTGCCTGAGAAACATAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 1695
1501 GCTGCTGAGAGAGATGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 1560
1696 GCTTCTCTGTGAGAGCGCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 1724
1561 GTTCTTCAATGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 1589

RESULT 7
HOMTNR 2087 bp mRNA linear PRI 10-NOV-1993
LOCUS Human tumor necrosis factor receptor mRNA, complete cds.
DEFINITION
ACCESSION M33294
VERSION M33294.1 GI:339744
KEYWORDS cell surface receptor; tumor necrosis factor receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 2087)
Schall, T.J., Lewis, M., Koller, K.J., Lee, A.L., Rice, G.C., Wong, G.H.,
Gatanga, T., Granger, G.A., Lenz, R., Raab, H., Kohl, W.J. and
Goeddel, D.V.
Molecular cloning and expression of a receptor for human tumor
necrosis factor
JOURNAL MEDLINE
Cell 61 (2), 361-370 (1990)
PUBMED 2158863

COMMENT Original source text: Human placenta, cDNA to mRNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by T. Schall, 26-MAR-1990.

FEATURES
Source
1. .2087
/organism="Homo sapiens"
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182..1549
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PELLR"

CDS
BASE COUNT 433 a 624 c 581 g 449 t
ORIGIN

Query Match 29.9%; Score 728.6; DB 9; Length 2087;
Best Local Similarity 69.7%; Pred. No. 1,6e-117;
Matches 1130; Conservative 0; Mismatches 399; Indels 92; Gaps 7;

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208 TACGGAGAGACGGTGTGTCTCATCTGTGCGGGCGGCACTGCCC-CAGCCCTATGGG 266
96 AGACCGAGTCCCGGAGAGCCCGAGCACTGCGCTGCGACACTGCCCCGAAATGGG 155
267 GGAATTGAGAGCCAGAGCTGCGCGGACATATGGGCTCCCCACCGTCTGCGCTGCTGCG 326
156 GGAGTGAAGAGCCATAGCTGTGCG-CATGGGCTCTCTCAACCTGCTGAGCTGCTGCTG 214
327 CCACTGTGTCTTCCAGCTCTGTGGCAAGTGTGTAACCCCGAGGGGTTCAAGGGCTGTGTC 386
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Db 1586 C 1586

RESULT 8
A43873 2175 bp DNA 11linear PAT 06-MAR-1997
LOCUS
DEFINITION Sequence 1 from Patent BP0657536.

ACCESSION A43873
 VERSION A43873.1 GI:2299022
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 2175)
 AUTHORS Wallach, D., Brackebusch, C., Varfolomeev, E. and Balkin, M.
 TITLE Proteases capable of shedding the soluble TNF-receptor and TNF-R derived peptides and antibodies against the proteases inhibiting the shedding
 JOURNAL Patent: EP 0657536-A 1 14-JUN-1995;
 YEDA RES & DBV (IL)
 COMMENT Other publication ZA 9407962 951121
 Other publication JP 7194376 950801
 Other publication AU 7574294 950504
 Other publication CA 2133872 950413.
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 BASE COUNT 474 a 641 c 604 g 456 t
 ORIGIN
 Query Match 29.8%; Score 727; DB 6; Length 2175;
 Best Local Similarity 69.6%; Pred. No. 3; Le-117;
 Matches 1123; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

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 Db 1360 TTGGCTGT 1419
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 Db 1540 GACTGT 1599

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Query 1746 C 1746
Db 1660 C 1660

RESULT 9
LOCUS A78738 2175 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 7 from Patent EP0568925.
ACCESSION A78738
VERSION A78738.1 GI:6090341
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2175)
AUTHORS Brakebush,C. and Wallach,D.
TITLE TNF RECEPTOR ACTION MODULATION
JOURNAL Patent: EP 0568925-A 7 10-NOV-1993;
YEDA RES & DEV (IL)
FEATURES
source 1.2175
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 474 a 641 c 504 g 456 t
ORIGIN

Query Match 29.8%; Score 727; DB 6; Length 2175;
Best Local Similarity 69.6%; Pred. No. 3.1e-117;
Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

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Db 529 TCAAAAAACACCTCAGACACTGCTCAGCTGTCTCAATATGCCAAAGAAATGGTCAAG 588
Query 627 GTGAGATTTTGGCTTGTGTAGTGAACGGGACACTGTGTGCGGTGTGAGAAACAG 686
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Query 1746 C 1746

Db 1660 C 1660

RESULT 10
AR041076

LOCUS AR041076 2175 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 1 from patent US 5811261.

ACCESSION AR041076

VERSION AR041076.1 GI:5961572

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2175)
Wallach, D., Nopnar, Y., Kemper, O., Engelmann, H., Brakebusch, C. and Aderka, D.

AUTHORS

TITLE Expression of the recombinant tumor necrosis factor binding protein 1 (TBF-1)

JOURNAL Patent: US 5811261-A 1 22-SEP-1998;

FEATURES
source 1..2175
location/Qualifiers

BASE COUNT 474 a 641 c 604 g 456 t

ORIGIN

Query Match 29.8%; Score 727; DB 6; Length 2175;
Best Local Similarity 69.6%; Pred. No. 3,1e-117;
Matches 112; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

QY 148 TGTCTCCGCGCCAGCTCTCAACCTTCACTCCCGACCCGAGGCCCGGCTCACTGGCA 207

Db 110 TCTCTATGCGCCGAGCTCAACCTTCACTCACTGACCCCAAGCACTTGGAGTCTTGAC 169

QY 208 TAGCGGAGACCGGTGTGTCTCACTGTCCGCGGCCCGCACTGCC-CAGCCCTGATGCG 266

Db 170 AGACCGAGTCCCGGAGAACCCACGACCTGCGCTGCACACTGACCTGAGCCCAATGCG 229

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QY 327 CCACTGTGCTTCCAGCTCTGTGTGCAAGATGTATACCCCGAGGGTTCAAGGGCTGCTC 386

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QY 387 CCTCACCCCGGCGGCGTGGAGAGAGAGAGTCCCTGTCCCAAGAAATATATACAC 446

Db 349 CCTCACCTTGGGCGAGAGAGAGAGATGTGTGTCTCCCAAGAAATATATATCCAC 408

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QY 1746 C 1746

Db 1660 C 1660

RESULT 11
164751

LOCUS 164751 2175 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 1 from patent US 5665859.
ACCESSION 164751
VERSION 164751.1 GI:2481645
KEYWORDS
SOURCE ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2175)
AUTHORS Wallach,D., Brakheusch,C., Varfolomeev,E. and Backlin,M.
TITLE Molecules influencing the shedding of the TNF receptor, their
preparation and their use
JOURNAL Patent: US 5665859-A 1 09-SEP-1997;
FEATURES Location/Qualifiers
source 1..2175
BASE COUNT 474 a 641 c 604 g 456 t
ORIGIN
Query Match 29.8%; Score 727; DB 6; Length 2175;
Best Local Similarity 69.6%; Pred. No. 3.1e-117;
Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;
148 TGTCCGCCGCCAGTCTCACTCTCACTCCCGACCCGAGGCCCGGCTCCACTGGCA 207
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1746 C 1746
DB 1660 C 1660

RESULT 12
LOCUS A26412 2111 bp DNA linear PAT 26-APR-1995
DEFINITION cDNA for (55KD TNF-BP) tumor necrosis factor binding protein from
patient EP0417563.
ACCESSION A26412
VERSION A26412.1 GI:904968
KEYWORDS
SOURCE Synthetic construct
ORGANISM Synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 2111)
 AUTHORS Brochhaus, M., Demic, Z., Gentz, R., Lesslauer, W., Loetscher, H. and
 Schlaeger, E. J.
 TITLE TNF-binding proteins
 JOURNAL Patent: EP 0417563-A 24 20-MAR-1991;
 F. HOFMANN-LA ROCHE AG
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RESULT 13
 AX409713 2111 bp DNA linear PAT 14-JUN-2002
 LOCUS AX409713
 DEFINITION Sequence 2360 from Patent WO0229103.

AUTHORS

Poulsen, H.S., Pedersen, N., Mortensen, S., Sorensen, S.B.,
 Petersen, M.W., and Eilander, H.I.
 Methods for identification of cancer cell surface molecules and
 cancer specific promoters, and therapeutic uses thereof
 Patent: WO 0300928-A 155 03-JAN-2003;
 Odin Medical A/S (DK)

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 445 a 629 c 587 g 450 t

ORIGIN

Query Match 29.74; Score 725.8; DB 6; Length 2111;
 Best Local Similarity 70.0%; Pred. No. 5e-117;
 Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

148 TGTCCCGCCCACTTCAACCTTCCATCCCGAACCCGAGCCCGGCTTCACTGGCA 207
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 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Loetscher, H., Pan, Y.C., Lahm, H.W., Gentz, R., Brockhaus, M.,
 Tabuchi, H., and Leeseleuer, W.
 Molecular cloning and expression of the human 55 kd tumor necrosis
 factor receptor.
 JOURNAL Cell 61 (2), 351-359 (1990)
 MEDLINE 90235284
 PUBMED 2158862

COMMENT Original source text: Human cell line HL60.. cDNA to mRNA.
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 Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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 747 GGCAAGTGAATATCCCTGCGAGAGAGACAGACACATCTGSCATCTGCATATGGGC 806
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· Tue Sep 16 09:11:45 2003

Search completed: September 15, 2003, 06:52:10
Job time : 6022 secs

us-09-970-532-1.rge

Page 19

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GenCore version 5.1.6
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OM nucleic - nucleic search, using ew model

Run on: September 15, 2003, 03:56:42 ; Search time 465 Seconds

(without alignments)
14164.793 Million cell updates/sec

Title: US-09-970-532-1

Perfect score: 2440

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	735.8	30.2	2141	11	ABQ77487
4	729.4	29.9	2141	11	AAQ06285
5	725.8	29.7	2088	12	AAQ01083
6	725.8	29.7	2088	22	AAQ03946
7	725.8	29.7	2111	20	AAQ09170
8	725.8	29.7	2111	22	AAH48859

9	725.8	29.7	2111	24	ABK84039
10	725.8	29.7	2111	24	ABN95862
11	725.8	29.7	2161	21	AAZ48475
12	725.8	29.7	2161	24	ABT04971
13	725.8	29.7	2161	24	ABK13194
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15	724.2	29.7	2111	12	AAQ010955
16	721.8	29.6	2062	13	AAQ020973
17	721.8	29.6	2062	13	AAQ024440
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19	719	29.5	2170	14	AAQ050870
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28	551	22.6	1334	11	AAQ06282
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30	543	22.3	543	24	ABQ79379
31	399.2	16.4	413	25	ABK37720
32	389.8	16.0	6889	17	AAT15931
33	388.6	15.9	6926	18	AAV04431
34	388	15.9	1335	25	ABT32043
35	377.8	15.5	1887	25	ABT32043
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37	366.8	15.0	1827	25	ABT32045
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ALIGNMENTS

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AC	AAAD42477;
XX	
DT	15-NOV-2002 (first entry)
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KW	Bovine, cattle; Coliform mastitis; inflammatory disease; receptor;
KW	tumour necrosis factor receptor-I; TNF-RI; antiinflammatory; Gene; ss.
XX	
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XX	
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Cytokine tumour ne
Human tumour necro
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Encodes human 55kD
TNF-alpha binding
Encodes TNF-alpha
Type I TNF recepto
p55 Tumour necrosi
Human TNF receptor
Lambda-derived TNF
Human TNFR1 coding
Rat sequence diffe
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Cytokine tumour ne
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Bovine tumour necr
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Bovine EST associa
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Concatameric immun
Concatameric immun
Encodes truncated
Concatameric immun
Encodes truncated
CADC-fusion polype
Target canine gene
cDNA for TBP(20-19
Human secretory TN
Human soluble tumo
Soluble tumour nec

PR 26-FEB-1999; 99US-122156P.
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
PA (USDA) US SEC OF AGRIC.
XX
XX Taylor MJ, Kehrl ME, Lee E;
PI MPI; 2002-58816/63.
DR P-Psdb; AAE25816.
XX
XX Novel nucleic acid molecule encoding bovine tumor necrosis factor
PT receptor-1 which is a potent inhibitor of tumor necrosis factor-alpha
PT useful for treating coliform mastitis or other inflammatory disease in
PT cattle
XX
XX Claim 1; Column 11-16; 16pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a polypeptide
CC that binds bovine tumor necrosis factor (TNF). The invention is useful
CC for expressing bovine TNF-R1 or soluble bovine TNF-R1 which is useful as
CC an inhibitor of TNF in cattle suffering from coliform mastitis or other
CC inflammatory disease. The nucleic acids and polypeptide or their
CC fragments are useful for treating mastitis. The present sequence is
CC bovine tumor necrosis factor receptor-1 (TNF-R1) cDNA.
XX
XX
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Query Match 100.0%; Score 2440; DB 24; Length 2440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1561 GGGCGGCGGCGAGCGCGCGGCGGAGGCAAGCTGGAAGCTGCGGGGCGGCGTCAAGG 1620
DB 1561 GGGCGGCGGCGAGCGCGCGGCGGAGGCAAGCTGGAAGCTGCGGGGCGGCGTCAAGG 1620
QY 1621 ACATGAGACTGCTGGGTTGCTTGAAGAAACATAGAGAGAGCGCTGGGTGCGCGCGCG 1680
DB 1621 ACATGAGACTGCTGGGTTGCTTGAAGAAACATAGAGAGAGCGCTGGGTGCGCGCGCG 1680
QY 1681 TCGGCTCGGAGCGCGCGCTTCTCTGTGTGAAGCCCGCGCTTCCGACTGCGGGCTCTCCG 1740
DB 1681 TCGGCTCGGAGCGCGCGCTTCTCTGTGTGAAGCCCGCGCTTCCGACTGCGGGCTCTCCG 1740

Oy		1741	CCCTGCACACGGCTGCTTCCTTCTGTGCCAGCAGCCCGAAGAATCTGGGAATGCC	1800
Db		1741	CCTTGCAACAACGGCTGCTTCCTTCTGTGCCAGCAGCCCGAAGAATCTGGGAATGCC	1800
Oy		1801	TGTGGACCTCCTGTTTGTGTTTTTTTCTGAGAGAAAGCTTGGAGNAGCAGCAC	1866
Db		1801	TGTGGACCTCCTGTTTGTGTTTTTTTCTGAGAGAAAGCTTGGAGNAGCAGCAC	1866
Oy		1861	GATCTGGAGGCAACTGACCTGCTGTACTCATCTAGTCAATAGCTTTTCTGAGTCCC	1920
Db		1861	GATCTGGAGGCAACTGACCTGCTGTACTCATCTAGTCAATAGCTTTTCTGAGTCCC	1920
Oy		1921	TGAGTGTGTCTGTGTGTAGTGTGTGTCTGCGTCCAGTCCGCTGTGTTGTGTCTGTA	1986
Db		1921	TGAGTGTGTCTGTGTGTAGTGTGTGTCTGCGTCCAGTCCGCTGTGTTGTGTCTGTA	1986
Oy		1981	TGTGCGTCTGTGTATGTGTGAGTGTGTGTACTCTGTGAGAGAGCCGAGTGTGCCGAGC	2040
Db		1981	TGTGCGTCTGTGTATGTGTGAGTGTGTGTACTCTGTGAGAGAGCCGAGTGTGCCGAGC	2040
Oy		2041	CCAAGGCACTGTGTGCGAAGATGAGAGGGGCGCCCTGCTTAATGCTGTTTTTGGGCTTG	2100
Db		2041	CCAAGGCACTGTGTGCGAAGATGAGAGGGGCGCCCTGCTTAATGCTGTTTTTGGGCTTG	2100
Oy		2101	GAGAACTGAGCAAGGCGCACTTGGGGAACCTTAGTGGTCCCTGAGCCGGTTCGACATG	2166
Db		2101	GAGAACTGAGCAAGGCGCACTTGGGGAACCTTAGTGGTCCCTGAGCCGGTTCGACATG	2166
Oy		2161	ATAAGCCATCTTTTGTATCTACCTCTTGCACTCACTCATCACTCTGTATCACTAAATAGAA	2220
Db		2161	ATAAGCCATCTTTTGTATCTACCTCTTGCACTCACTCATCACTCTGTATCACTAAATAGAA	2220
Oy		2221	CTTTGTGCCCCCTGCTGTGACCAAGCTGAACTGTCCCCCAGGCAAGCGGGGAGACAGAAAA	2286
Db		2221	CTTTGTGCCCCCTGCTGTGACCAAGCTGAACTGTCCCCCAGGCAAGCGGGGAGACAGAAAA	2286
Oy		2281	TGGGGCTCCCCAAGGAGACTAGCTGTTCAGTTCAAGTTCAGTTCGCTCAGTCCGTCCGACT	2346
Db		2281	TGGGGCTCCCCAAGGAGACTAGCTGTTCAGTTCAAGTTCAGTTCGCTCAGTCCGTCCGACT	2346
Oy		2341	CTTTGCGACCTCTGTGATATCGACAGGACCTTGTGTAAATACATAAATCTTCCAAATTAAAG	2400
Db		2341	CTTTGCGACCTCTGTGATATCGACAGGACCTTGTGTAAATACATAAATCTTCCAAATTAAAG	2400
Oy		2401	CTCTGCCCTGAGGGCACTGTTAAAAAAAAAAAAAAAAAAAAA 2440	
Db		2401	CTCTGCCCTGAGGGCACTGTTAAAAAAAAAAAAAAAAAAAAA 2440	

RESULT 2
ABQ79378 standard; cDNA, 2440 BP.

ID ABQ79378;
XX ABO79378;
XX
DT 05-NOV-2002 (first entry)
XX
DB Bovine tumour necrosis factor receptor-1 cDNA.
DE
XX Bovine; tumour necrosis factor receptor-1; TNF-R1; antiinflammatory;
KW TNF cytotoxicity; mastitis; tumour necrosis factor-alpha; TNF-alpha;
RW monoclonal antibody BC9; TNF-beta; gene; ss.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
FT CDS . 294..1709 /*tag= a
FT sig_peptide . 294..383 /*product= "Bovine TNF-R1"
FT /*tag= b
FT /label= signal_peptide

FT	mat_peptide	384..1706
FT	/tag= C	
FE	/label= mature_bovine_TNF-R1	
XX		
PN	US2002076765-A1.	
PD	20-JUN-2002.	
PE	03-OCT-2001; 2001US-0970532.	
PR	26-FEB-1999; 99US-122156P.	
PR	25-FEB-2000; 2000US-0513007.	
PA	(IOWA) UNIV IOWA STATE RES POUND INC.	
XX		
PI	Taylor MJ, Kehrl ME, Lee E, Mwangi S;	
DR	WPI; 2002-557247/59.	
DR	P-PSDB; ABB98169.	
XX		
PT	New isolated, soluble, bovine tumour necrosis factor receptor 1, useful	
PT	for inhibiting tumour necrosis factor cytotoxicity for treating	
PT	mastitis, is a better inhibitor of tumour necrosis factor compared to	
PT	monoclonal antibody BC9 -	
XX		
PS	Claim 1(a); Fig 1; 17pp: English.	
XX		
CC	The invention relates to an isolated nucleic acid encoding bovine tumour	
CC	necrosis factor receptor-1 (TNF-R1). The activity of polynucleotides of	
CC	the invention may be described as antiinflammatory. Polypeptides of the	
CC	invention are useful for inhibiting TNF cytotoxicity in a bovine. This is	
CC	useful for treating mastitis and other inflammatory disease. Soluble	
CC	bovine TNF-R1 is a better inhibitor of bovine TNF-alpha than monoclonal	
CC	antibody BC9 (an antibody directed towards TNF-alpha), and can bind both	
CC	TNF-alpha and TNF-beta. The current sequence represents bovine tumour	
CC	necrosis factor receptor-1 cDNA.	
XX		
SQ	Sequence 2440 BP, 441 A; 771 C; 701 G; 527 T; 0 other;	
	Query Match	100.0%; Score 2440; DB 24; Length 2440;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 2440; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 TTTTATTTTTTTTTTTCTTTTTGGGCGGAAGGGTGACCCCTTCCTCCCACC	60
DB	1 TTTTATTTTTTTTTTTCTTTTTGGGCGGAAGGGGTGACCCCTTCCTCCCACC	60
OY	61 TCCTCTCAGCTCAAGTTTTCTCGAGCTCTTCGGGCTTGAGGCCGAGGCTGGGCTTCC	120
DB	61 TCCTCTCAGCTCAAGTTTTCTCGAGCTCTTCGGGCTTGAGGCCGAGGCTGGGCTTCC	120
OY	121 GGATTGAGGCTCTCCGGATTGGGCTGTGTCCGCCTCAGCTTCAACCTTCACCTCCC	180
DB	121 GGATTGAGGCTCTCCGGATTGGGCTGTGTCCGCCTCAGCTTCAACCTTCACCTCCC	180
OY	181 GACCCGAGGCCCGGAGCTTCACCTGAGGCAATAGCGAGAGCACCTGTGTCTACTGTGCGGG	240
DB	181 GACCCGAGGCCCGGAGCTTCACCTGAGGCAATAGCGAGAGCACCTGTGTCTACTGTGCGGG	240
OY	241 GCGCGCACTGCCCGAACCTGTAAATGGGGGATTGAGAAGGCACAAGCTGGGCCGACATGGGCC	300
DB	241 GCGCGCACTGCCCGAACCTGTAAATGGGGGATTGAGAAGGCACAAGCTGGGCCGACATGGGCC	300
OY	301 TCCCCACTGGTCTGGGCTGGCTGCTGCACATGTGTCTTCAAGCTCTGTGGCAGATGTGT	360
DB	301 TCCCCACTGGTCTGGGCTGGCTGCTGCACATGTGTCTTCAAGCTCTGTGGCAGATGTGT	360
OY	361 ACCCGCAGAGGGGTTCAAGGGGCTGTCTCCCTCACCCCGGGACCTGGAGAGAGAGACTC	420
DB	361 ACCCGCAGAGGGGTTCAAGGGGCTGTCTCCCTCACCCCGGGACCTGGAGAGAGAGACTC	420
OY	421 CCTGTCCCCAAGAAAATAACCAACCGCAAAATAGACCATTTGTCTGCACCAAGTGC	480
DB	421 CCTGTCCCCAAGAAAATAACCAACCGCAAAATAGACCATTTGTCTGCACCAAGTGC	480

Db 421 CCTGTCCCAAGAAATATTAACACCCCGAAATAGCAACATTTGTGACCAAGTCC 480
 Qy 481 ACAAAGTACCTATCTGTACATGACTGTCCGGGTCCAGGGGAGACAGGACTGCAGG 540
 Db 481 ACAAAGTACCTATCTGTACATGACTGTCCGGGTCCAGGGGAGACAGGACTGCAGG 540
 Qy 541 TGTGTGCCCCCTGGCACTTGTACACTGCTTGGAGAACATCTCAGACAGATGCTGAGCTCT 600
 Db 541 TGTGTGCCCCCTGGCACTTGTACACTGCTTGGAGAACATCTCAGACAGATGCTGAGCTCT 600
 Qy 601 CCAGGTCCGGGACGAAATGTTCCAGGTGAGATTTCCCTTGTGTAGTGAACCGGACA 660
 Db 601 CCAGGTCCGGGACGAAATGTTCCAGGTGAGATTTCCCTTGTGTAGTGAACCGGACA 660
 Qy 661 CTGTGTGGGCTGCGAGAAACAGTACCGGGAATATCTGGGGTGAACCTGGCTCCGGT 720
 Db 661 CTGTGTGGGCTGCGAGAAACAGTACCGGGAATATCTGGGGTGAACCTGGCTCCGGT 720
 Qy 721 GTCTGAACCTGAGCCTCTGTCCCAATGGCACAGTGAATATCCCTGCGAGAGACAG 780
 Db 721 GTCTGAACCTGAGCCTCTGTCCCAATGGCACAGTGAATATCCCTGCGAGAGACAG 780
 Qy 781 ACACCATCTGCGACCTGCTGCAATATGAGCTTCTTTTAAAGCGGCAAGTGCATCTCTGTC 840
 Db 781 ACACCATCTGCGACCTGCTGCAATATGAGCTTCTTTTAAAGCGGCAAGTGCATCTCTGTC 840
 Qy 841 ATGATTTGAAGAACAGAGAGTGGAGAGTTATGTCCAAACCCGACTTCACTGGTAAAG 900
 Db 841 ATGATTTGAAGAACAGAGAGTGGAGAGTTATGTCCAAACCCGACTTCACTGGTAAAG 900
 Qy 901 ACTCTCAGAGACCAAGGACCTACAGTACTATTACCCCTGGTGAATTTCTTCCGGCTTTGCC 960
 Db 901 ACTCTCAGAGACCAAGGACCTACAGTACTATTACCCCTGGTGAATTTCTTCCGGCTTTGCC 960
 Qy 961 TGGCATCTTGGCCTCTGTGCTTGTAGCATGCTGTACAGGGGTGAAGGCCAAGCTCT 1020
 Db 961 TGGCATCTTGGCCTCTGTGCTTGTAGCATGCTGTACAGGGGTGAAGGCCAAGCTCT 1020
 Qy 1021 ACTGCATCATTTGGGGGAGTGGACTGTGTAAAGAGGGGAGCCAAACCTCGTGCTC 1080
 Db 1021 ACTGCATCATTTGGGGGAGTGGACTGTGTAAAGAGGGGAGCCAAACCTCGTGCTC 1080
 Qy 1081 CGGCCCCAGGCTTCAACCCCAACACACCATCTGCTTCAAGCTTCAAGCTTCAAGCT 1140
 Db 1081 CGGCCCCAGGCTTCAACCCCAACACACCATCTGCTTCAAGCTTCAAGCTTCAAGCT 1140
 Qy 1141 CTGTCTCCATTCCCTTACATCTCTGTGACCGGCTCAACTTGGAGCCGCTGCACTCTC 1200
 Db 1141 CTGTCTCCATTCCCTTACATCTCTGTGACCGGCTCAACTTGGAGCCGCTGCACTCTC 1200
 Qy 1201 CCTCCAGGAGAGCGGCCCCGACCTTAAGGCTGGGCCCATCTCCCGGGGCTCCGG 1260
 Db 1201 CCTCCAGGAGAGCGGCCCCGACCTTAAGGCTGGGCCCATCTCCCGGGGCTCCGG 1260
 Qy 1261 CCTCCAGGAGAGCGGCCCCGACCTTAAGGCTGGGCCCATCTCCCGGGGCTCCGG 1320
 Db 1261 CCTCCAGGAGAGCGGCCCCGACCTTAAGGCTGGGCCCATCTCCCGGGGCTCCGG 1320
 Qy 1321 CTTCGGGCTCCACCACTCTGTGACACCCAGATTGAGAGTGGAGGCCAGGCCCAAGC 1380
 Db 1321 CTTCGGGCTCCACCACTCTGTGACACCCAGATTGAGAGTGGAGGCCAGGCCCAAGC 1380
 Qy 1381 CCCCCGATCAGCTGCGGATGCGGACCCCGGACCTCTGAAGCGGCTGGTGAACGGCGTGC 1440
 Db 1381 CCCCCGATCAGCTGCGGATGCGGACCCCGGACCTCTGAAGCGGCTGGTGAACGGCGTGC 1440
 Qy 1441 CCCCCGATCAGCTGCGGATGCGGACCCCGGACCTCTGAAGCGGCTGGTGAACGGCGTGC 1500
 Db 1441 CCCCCGATCAGCTGCGGATGCGGACCCCGGACCTCTGAAGCGGCTGGTGAACGGCGTGC 1500
 Qy 1501 GGCTGTGAGCTGAGAACGGGCGCCACCTGCGGAGGCGCAGTACAGCATGCTGGCGGCT 1560
 Db 1501 GGCTGTGAGCTGAGAACGGGCGCCACCTGCGGAGGCGCAGTACAGCATGCTGGCGGCT 1560

Qy 1561 GGCGGCGGCGCAGCGCGCGCGGCGAGGCGACGCTGAGCTGTGGGGCGGCTGCAGG 1620
 Db 1561 GGCGGCGGCGCAGCGCGCGCGGCGAGGCGACGCTGAGCTGTGGGGCGGCTGCAGG 1620
 Qy 1621 ACATGAGCTGCTGGTGGTCTGTGAAACATAGAGAGGCGCTGGTGGCGCGCGCGC 1680
 Db 1621 ACATGAGCTGCTGGTGGTGGTCTGTGAAACATAGAGAGGCGCTGGTGGCGCGCGCGC 1680
 Qy 1681 TCGGCTCCGAGCCCGGCTTCTGTGTGAGAGCCCGCGCTCCGACTGCGGGCTCCCG 1740
 Db 1681 TCGGCTCCGAGCCCGGCTTCTGTGTGAGAGCCCGCGCTCCGACTGCGGGCTCCCG 1740
 Qy 1741 CCGTGCAGAGCGGCTTCCCTCTGTGCGCAGGAGCCCGGAAAGATCTGAGAGTGC 1800
 Db 1741 CCGTGCAGAGCGGCTTCCCTCTGTGCGCAGGAGCCCGGAAAGATCTGAGAGTGC 1800
 Qy 1801 TGTGACCTCCTGTTTTGTTTTGTTTTTCTGAGAGAGAGCTTGGAGAGAGAGCAG 1860
 Db 1801 TGTGACCTCCTGTTTTGTTTTGTTTTTCTGAGAGAGAGCTTGGAGAGAGAGCAG 1860
 Qy 1861 GATCTGCGAGCACTGACCTGTGCTACTACTAGTGTACATAGCTTTTCTCAGCTGCC 1920
 Db 1861 GATCTGCGAGCACTGACCTGTGCTACTACTAGTGTACATAGCTTTTCTCAGCTGCC 1920
 Qy 1921 TGAAGTGTGTCTGT 1980
 Db 1921 TGAAGTGTGTCTGT 1980
 Qy 1981 TGTGCGTCTGT 2040
 Db 1981 TGTGCGTCTGT 2040
 Qy 2041 CCAAGGCAAGT 2100
 Db 2041 CCAAGGCAAGT 2100
 Qy 2101 GAGAACTCAGCAAGGCGACTTGGGGAACCTTACGTCCGCTCCGAGCGGCTTCCAGTAG 2160
 Db 2101 GAGAACTCAGCAAGGCGACTTGGGGAACCTTACGTCCGCTCCGAGCGGCTTCCAGTAG 2160
 Qy 2161 ATTAAGCATCTTTGTATCCACTGTGACATCACTCACTCACTCACTCACTCACTCACT 2220
 Db 2161 ATTAAGCATCTTTGTATCCACTGTGACATCACTCACTCACTCACTCACTCACTCACT 2220
 Qy 2221 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
 Db 2221 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
 Qy 2281 TGGGGGCTCCCAAGGAGCTGAGTTCAGTTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGT 2340
 Db 2281 TGGGGGCTCCCAAGGAGCTGAGTTCAGTTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGT 2340
 Qy 2341 CTTTGCAGCCTGTGAAATCGAGGAGCTTCTGTAAATACATAAATCTTCAATTAAG 2400
 Db 2341 CTTTGCAGCCTGTGAAATCGAGGAGCTTCTGTAAATACATAAATCTTCAATTAAG 2400
 Qy 2401 CTCTGCTGTGAGGAGCTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2440
 Db 2401 CTCTGCTGTGAGGAGCTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2440

RESULT 3
 AB077487
 ID AB077487 standard; DNA; 2141 BP.
 AC AB077487;
 XX 14-MAY-2003 (first entry)
 DT Human TNF-R DNA huTNF-R.
 DE Human TNF-R DNA huTNF-R.
 XX TNF, human; tumour necrosis factor; tumour necrosis factor receptor;
 KM

KM TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour; gene; ds.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT 213..1580
 FT CDS /tag= a
 FT /product= "huTNF-R"
 EP93438-A.
 XX
 XX 24-OCT-1990.
 PD
 PF 06-APR-1990; 90EP-0106624.
 XX
 XX 21-APR-1989; 89DE-3913101.
 PR 21-JUN-1989; 89DE-3920282.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (STND) SYNERGEN INC.
 PI Hauptmann R, Himmler A, Maurer-Fogy I, Stralowa C;
 XX
 XX WPI: 1990-321987/43.
 DR P-PSDB: ABG74755.
 XX
 PT DNA encoding TNF binding protein and TNF- receptor - used in tumour
 XX treatment and to understand mechanisms to TNF action
 XX
 PS Example 9; Fig 9; 51pp; German.
 CC This invention describes novel polynucleotide sequences encoding tumour
 CC necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).
 CC The products of the invention are useful in pharmaceutical compositions
 CC for prophylaxis or treatment of human tumours and to understand the
 CC mechanisms of TNF action. This sequence encodes the human TNF-R.
 CC huTNF-R described in the disclosure of the invention.
 XX
 XX Sequence 2141 BP; 455 A; 634 C; 592 G; 460 T; 0 other;
 SQ
 Query Match 30.2%; Score 735.8; DB 11; Length 2141;
 Best Local Similarity 69.9%; Pred. No. 4.5e-141;
 Matches 1152; Conservative 0; Mismatches 402; Indels 95; Gaps 8;

Db 436 CGGGCAGAGATACGAGCTGACGAGGAGTGAGAGCCGCTCTTCAACGCTTCAGAAAAACC 495
 Qy 577 ATCTCAGACGATGCTGAGCTGCTCCAGTGCCGGGAGCAAAATGTTCCAGGTGAGATT 636
 Db 496 ACCTCAGACGATGCTGAGCTGCTCCAGTGCCGGGAGCAAAATGTTCCAGGTGAGATT 555
 Qy 637 CGCTTGTGTAGTGTGAGACCGGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 696
 Db 556 CTTCCTCAGACGATGAGCGGAGCACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 615
 Qy 697 ACTGGGGTGAACCTGGCTTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 756
 Db 616 ATTGAGGTGAACCTTTTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 675
 Qy 757 ATATCCCTGCGCAGAGAGACAGAGACCAATCTGCACTGCAATATGAGGCTTTCTTTCTTA 816
 Db 676 ACCTCTCTGCGCAGAGAGACAGAGACCAATCTGCACTGCAATATGAGGCTTTCTTTCTTA 735
 Qy 817 AAGGCGCCAAAGTGCATCTCTGTGATGATTGTAAAGAA---CAAGAGTGTGAGAAATTAT 873
 Db 736 GAGAAACGAGTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 795
 Qy 874 GTCCAACTCCGACCTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933
 Db 796 GCTTACCCCAAGT 855
 Qy 934 CCGT 993
 Db 856 CCTGT 915
 Qy 994 GTTACCAAGCGGT 1053
 Db 916 GCTTACCAAGCGGT 975
 Qy 1054 AAGGCGCGGAGCGCAAGAA-----CTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1104
 Db 976 AAGGCGCGGAGCGCTTGAAGAACTTACTTAAAGCCCTGCGCCCAACCAAGCTTCACTC 1035
 Qy 1105 CCACCATCTGCTGAGT 1164
 Db 1036 CCACTTCAAGGCTTGT 1095
 Qy 1165 CTTGT 1215
 Db 1096 CCACTTCAAGGCTTGT 1155
 Qy 1216 CCGGCGCCCATTTAAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1275
 Db 1156 CACCACTTATCAAGGCGGT 1186
 Qy 1276 GTACCCCGGGGCTTCCGCGCTTCAACCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 1335
 Db 1187 -----TGGCAAGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1209
 Qy 1336 ACCTTGTACACCCGATTCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1395
 Db 1210 CCAATCCCAACCCCTTCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1266
 Qy 1396 CGAGT 1455
 Db 1267 ACACTGT 1326
 Qy 1456 AGGAGT 1515
 Db 1327 AGGAGT 1386
 Qy 1516 ACAGGCGCCCACTTGT 1575
 Db 1387 ACAGGCGCCCTGT 1446
 Qy 1576 CGGCGCGGAGCGCACTGT 1635


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Db      862 TTAATGATTCCTACCAACGGTGAAGTCAAGCTTACTCTATGTTGTTGGAAATCG 921
Qy      1044 ACTCTGTAAAGAGGGAGGAGCCAGAA-----CTCTGGTCCGGGCCCCAGGCTTC 1094
Db      922 ACACCTGAAAAAGAGGGAGCTTGAAGAACTACTACTAAGCCCTGGCCCCAAACCA 981
Qy      1095 AACCCCAACCAACCATCTGCTTTCAGCTCCACCCCAAGTTCCAGTCTCTCTCCATTCC 1154
Db      982 AGCTTCACTCCACCTCAGAGGCTTCAACCCCACTCGGGCTTCAAGTCCGTCAGATTCC 1041
Qy      1155 CCTTACATCTCTCTGACCGGTCCAACTTCGAG-----CCGTGCATCTCCCTCC 1205
Db      1042 ACCTTCACTCCAGCTCACTATACCCCGGTACTCTCCCACTTTCGGCTCCCGC 1101
Qy      1206 AGCAGACGCGCCCGCCCTATTAAGGCTGAGCCCTCTCCGGGCTTCGGGCTCC 1265
Db      1102 AGAGAGGTGGCAACCACTATCAGGGGGCTGACCCCATCT----- 1142
Qy      1266 ACCCACTCTGTAACCCCGGGCTCCGGGCTTCACCCCACTCTGTACCCCGGGGCTCCG 1325
Db      1143 -----TGCAACAGCCTTC 1155
Qy      1326 GCCTTCAACCACTCTGCAACCCCAAGTTGAAAGTGGAGCCAGCGCCCAAGCGCCCC 1385
Db      1156 GCCTTCAACCCCACTCTGCAACCCCTTCAAGAGTGGAGAGAGGCCCAACA--AGCCA 1212
Qy      1386 GATCAGCTCGGAGATCGGACCCCGCAACCTGTACCGCGTGTGAGACGGCGTCCCG 1445
Db      1213 CAGAGCTTGAACACTGATGACCCCGCGCAAGCTGTACCGCGTGTGAGAACCTGCCCCG 1272
Qy      1446 TCGGCTTGAAGAGATTGTGCGGGGCTGGAGCTGAGCGAGCAAGATGAGAGGCTG 1505
Db      1273 TTGCGCTGAAGAAATGTGTGGGCGCTTGAAGGCTGACGAGCAAGAAATGATGCGCTG 1332
Qy      1506 GAGCTGAGAAAGGAGCGGCGCACTGCGGAGGCGAGGAGTACAGATCTGCGGCGCTGCG 1565
Db      1333 GAGCTGAGAAAGGAGCGGCGCTGCGGAGGCGCAATACAGATCTGCGCACTGAGAG 1392
Qy      1566 CGGCGGACCGCGCGCGCGAGGCGCAAGTGAAGCTGTGGCGCGCTGCTCAAGGACATG 1625
Db      1393 CGGCGGACCGCGCGCGCGAGGCGCAAGTGAAGCTGTGGCGCGCTGCTGCGCAATG 1452
Qy      1626 GACCTGTGGGTTGCTGGAAGAAATAGAGAGGAGGCTGGTGGGCGCGCGCGCTGCG 1685
Db      1453 GACCTGTGGGTTGCTGGAAGAAATAGAGAGGAGGCTGGTGGGCGCGCGCGCTGCG 1512
Qy      1686 TCCGAGCCCGGCTTCTCTGTGAAGCCCGGCGCTCCG 1724
Db      1513 CCGCGGCCCAAGCTTCTCAGATGAGGCTGGCGGCGCTCCG 1551

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RESULT 6
AAC83946
ID AAC83946 standard; DNA; 2088 BP.

AC AAC83946;

DT 02-MAR-2001 (first entry)

DE Human 30 kDa TNF inhibitor precursor coding sequence.

XX TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;

XX IL-1; inflammatory disease; degenerative disease; human; 88.

XX Homo sapiens.

XX US6143866-A.

XX 07-NOV-2000.

XX 19-JAN-1995; 95US-0375242.

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PR 19-JUL-1990; 90US-0555274.
PR 09-JUL-1993; 93US-0090366.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
PA (AMGE-) AMGEN INC.
XX Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
P1 Vanderbilt RW, Vannice J, Kohno T;
XX MPI: 2001-006443/01.
DR P-PSDB; AAB37677.
XX
PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF.
XX
XX Example 6; Fig 21; 82bp; English.
XX
CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC novel TNF inhibitors of the present invention are useful as therapeutic
CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC for treating inflammatory and degenerative diseases mediated by TNF. The
CC present sequence is the coding sequence for the precursor of 30 kDa TNF
CC inhibitor. The 30 kDa TNF inhibitor can inhibit TNF alpha.
XX
SQ Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;

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Query Match 29.7%; Score 725.8; DB 22; Length 2088;

Best Local Similarity 70.0%; Pred. NO. 5e-139; Mismatches 387; Indels 92; Gaps 7;

Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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Qy 148 TGTCCCGGCCCCAGTCTCAACCTTCACCTCCCGAGCCGAGGCCGCTTCACTGGCA 207
Db 23 TCTTATGCCCCGAGATCTCAACCTTCACCTTCACCCCAAGCACTTGGAGAGCTGGAC 82
Qy 208 TACCGAGAACCGTGTGTCTCTCACTGTGCGGGCGGCACTGCC--CAGCCCTGATGGG 266
Db 83 AGACCGAGTCCCGGAGAGCCCGACACTGCGCGTCCCACTGCGCTGAGGCCAATAGGG 142
Qy 267 GGATTGAGAGGCGACAGTGGCGGAGATAGGAGCTCCCAAGGCTGCGCTGCTGCTG 326
Db 143 GAGTGAAGGCGCATAGCTGTCTGG--CATGGGCTCTTCACCGTGTGCTGCTGCTG 201
Qy 327 CCACTGTGCTTCCAGCTCTGTTGGAGATGTATACCCCGAGGGATTCAAGGGCTGCTC 386
Db 202 CCGCTGGTGTCTCTGAGAGCTGTGTGGAAATATACCTTCAGGGATTATGACTGCTC 261
Qy 387 CCTCACCCCGGAGACCTGAGAGAGAGAGAGTCCCTGTCCCAAGGAAATATACAC 446
Db 262 CCTCACCTAGGGGAGAGGAGAGAGATGTGTGTGTCTCCCAAGGAAATATATCAC 321
Qy 447 CCGCAAAATACACCATTTGTGTGACCAAGTGCACAAAGGTACTATCTGTACATGAC 506
Db 322 CTTCAAAATATTTGATTTGCTGTACAGTGCACAAAGGAACTTATACATATAC 381
Qy 507 TGTCCGGTTCAGGGCGAGACAGGAGTGAAGTGTGTGCGCTGAGCACTACATGCC 566
Db 382 TGTCCAGGCGCGGGGAGAGATACGAGTGAAGAGTGTGAGAGCGGCTTTCACGCT 441
Qy 567 TTGAGAACCATCTCAAGCATGCTTGAAGTGTCTCAAGTGTCCGAGAGCAAAATGTTCCAG 626
Db 442 TCAGAAAACCACTCAGCACTGCTCAGCTGTCCAAATGCCAAGAAATATGGGTAG 501
Qy 627 GTGAGATTTCGCGCTTGTGTGAGACCGGAGACCTGTGTCGCGTGCAGAGAAACAG 686
Db 502 GTGAGATCTTCTTTCAGACGTGACCGGAGACCGTGTGTGCTGAGAGAAACAG 561
Qy 687 TACCGGAAATCTGGGAGTGAATGGCTTCCGGTGTCTGAATCGACGCTGTCTCCAT 746

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Db 562 TACCGGCAATTATGAGTGAACCTTTTCAGTCTTCAATTGACGCTCTGCTCAAT 621
Qy 747 GGCACAGTAATAATCCCTGTCAGAGAGACAGGACACCAATCTGCAATATGAGC 806
Db 622 GGGACCGTGAACCTCTCTCCAGAGAAACAGAACCGCTGACCTCCATGACGT 681
Qy 807 TTTCTTTTAAAGCGCCAAAGTCATCTCTGTCATGATTGTAAGAA--CAAGAGTCG 863
Db 682 TTTCTTTTAAAGAAACAGAGTGTCTCTGTCATGTAAGAAACCTGAGATGC 741
Qy 864 GAAAGATATGTCCACCCGACCTTCAACGTGTAAGATCTTCAGGACCCAGGACTACA 923
Db 742 ACCAAGTTGGCTTACCCAGATTGAAGATGTAAGGCACTGAGCACTAGGACACA 801
Qy 924 GTACTATTACCCCTGATGTTCTTCTGAGCTTCTGCTGAGCATCTTGCCTCTGCTC 983
Db 802 GTGCTGTGGCCCTGGTCACTTTTCTTGGTCTTCTTATCCCTCTCTTCAATGGT 861
Qy 984 TTAGCATGTGCTACAGCGGTGAGAGCCCAAGCTTACTTCATCAATTTGCGGAGTCG 1043
Db 862 TTATGATGCTACCAACGCTGAGAGTCCAGCTTACTTCTGTTTGGGAAATCG 921
Qy 1044 ACTCTGTAAAGAGGGGAGCCAGAA-----CTCTGCTCCGCGCCCGAGGCTTC 1094
Db 922 ACACCTGAAAAAGGAGGAGCTTGAAGAACTAATAAGCCCTGAGCCCAACCCA 981
Qy 1095 AACCCACACACACATCTGCTTCAAGCTCCACCCCAAGTTCCAGTCTCTCATTC 1154
Db 982 AGCTTCACTGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1041
Qy 1155 CTTTACATCTCTGCTGACCGGTCCAACTTTCGAG-----CGGTGCACTCTCTCC 1205
Db 1042 ACCTTCACTGCTGACCTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 1101
Qy 1206 AGGAGAGCGGCGCGCGCGCTTAAAGCTGAGCTGCTCCGCGGCGCTCCGCTCC 1265
Db 1102 AGAGAGGTGAGCAACCTTATGAGGAGGAGCTGAGCTTCAAGCTTCAAGCT 1142
Qy 1266 ACCACCTGCTGACCGCGGCGCTCCGCGCTTCAAGCTTCAAGCTTCAAGCT 1325
Db 1143 -----TGCCACAGCCCTC 1155
Qy 1326 GCTTCCACCACTCTGCAACCCAGTTCAAGATGAGAGAGCCAGCGCGCGCGCC 1385
Db 1156 GCTTCCACCACTCTGCAACCCAGTTCAAGATGAGAGAGCCAGCGCGCGCGCC 1212
Qy 1386 GATGAGCTGCGGATGCGGACCGCGGACCTCTGATGAGGAGGAGGAGGAGG 1445
Db 1213 CAGAGCTTGAACACTGATGACCGCGGACCTGATGAGGAGGAGGAGGAGG 1272
Qy 1446 TCGGCTGGAAGAGTTGTTGCGGCGGCTGAGGACCTGAGCGAGCAAGATGAGCG 1505
Db 1273 TTTGGCTGGAAGAGTTGTTGCGGCGGCTGAGGACCTGAGCGAGCAAGATGAG 1332
Qy 1506 GAGCTGGAAGAGCGGCGGACCTTCCGCGAGCGAGGATGACAGATGCTTGGCG 1565
Db 1333 GAGCTGGAAGAGCGGCGGCTGCTGCGAGGCGCAATACAGATGCTTGGCGAG 1392
Qy 1566 CGGCGGACCGCGCGCGGAGGCGCAAGCTGAGGCTGCGGCGCGCTGCTGAG 1625
Db 1393 CGGCGGACCGCGCGCGGAGGCGCAAGCTGAGGCTGCGGCGCGCTGCTGAG 1452
Qy 1626 GACCTGCTGAGTTGCTGGAAGAAACATAGAGAGGAGGCTGGTGGGCGCGCGCT 1685
Db 1453 GACCTGCTGAGTTGCTGGAAGAAACATAGAGAGGAGGCTGGTGGGCGCGCGCT 1512
Qy 1686 TCCGAGCGCGCGCTTCTCTGTTGAAGCGCGCGCGCTCCG 1724
Db 1513 CCGCGCGCGCGAGTCTTCTCAATGAGGCTGCGCGCGCTCCG 1551

ID AA209170 standard; cDNA; 2111 BP.
AC XX
XX AA209170;
AC XX
XX 20-MAR-2003 (updated)
DT 18-OCT-1999 (first entry)
DE XX
XX Human tumour necrosis factor binding protein cDNA.
KM Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KM anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KM autoimmune glomerulonephritis; cerebral malaria; immune response;
KM antagonist; diagnosis; de.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 187..1554
FT /cag= a
FT /product= "TNF binding protein"
FT sig_peptide 187..273
FT /*cag= b
FT mat_peptide 274..1551
FT /*cag= c
FT
FT
XX EP39121-A2.
XX
XX 01-SEP-1999.
XX
XX 31-AUG-1990; 99EP-0100703.
XX
XX 12-SEP-1989; 89CH-0003319.
XX 08-MAR-1990; 90CH-0000746.
XX 20-APR-1990; 90CH-0001347.
XX 31-AUG-1990; 90EP-0116707.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;
XX WPI; 1999-480840/41.
XX P-PSDB; AAY30934.
XX
XX New insoluble proteins, and fragments, that bind to tumor necrosis
PT factor, used to treat e.g. septic shock or cerebral malaria
XX
XX
XX Claim 4, Fig 1; 25pp; German.
XX
XX This invention describes novel homogeneous insoluble proteins (I),
CC their (in)soluble fragments (Ia) and their salts that can bind tumour
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence encodes
CC a tumour necrosis factor binding protein described in the method of
CC the invention.
CC (Updated on 20-MAR-2003 to correct PF field.)
CC (Updated on 20-MAR-2003 to correct PR field.)
CC
XX
SQ Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;

Query Match 29.7%; Score 725.8; DB 20; Length 2111;
Best Local Similarity 70.0%; Pred. No. 5e-139;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

Qy 148 TGTCCCGCGCGAGTCAACCTCCCACTCCCGAGCCGAGGCGCGGCTCCAGTGGCA 207
Db 41 TCTTATCCCGAGTCAACCTCCCACTCCCGAGCCGAGGCGCGGCTCCAGTGGAC 100

OY	208	TACGAGGAGACGGTGTGTGTGTCACTGTGTGGCGGGCGGCACTGCC-CAGCCCTTAATGGG	266
Db	101	AGACCGAGTCCCGGGAAGCCCAAGCACTGCCGTGTCAACATCGCTTGAGGCCCAATAGGG	160
OY	267	GGATTGAGAGGCGACAGCTGAGCGGACATGGGCTTCCCAACGGTGTGACCTGTGCTG	326
Db	161	GGAGTGAAGGCGCATATAGCTGTCTGG-CATGGGCTCTTCCACCGTGTCACTCGTGGCTG	219
OY	327	CCACTGGTGTCTTCCAGCTCTGTTGGCAATGTGTACCCCGGAGGGGTTTACGGGGCTGGTC	386
Db	220	CGGCTGGTGTCTCTGAGCTGTGGGGAATATACCCCTTCAGGGGGTATTTGAACTGGTGC	279
OY	387	CCTCACCCCGGGAGCTGTGAGAGAGAGAGAGTCCCTGTGCCCAAGSAAATATATACAC	446
Db	280	CCTCACTTAGGGGACAGGGAAGAGAGATATGTGTGTGCCCAAGSAAATATATATCCAC	339
OY	447	CCGCAAAATAGCAACCATTTTGTCTGCACCAATGTGCCCAAGGTAACCTATCTGTACATGAC	506
Db	340	CCTCAAAATATATTCGATTTGTCTGTACCAATGCCCAAGGTAACCTATCTGTACATGAC	399
OY	507	TGTCGGGGTCCAGGGCGAGACACGGGACTGCAAGGATGTGGGCTTGGCCCTGGGCACTACCTGCC	566
Db	400	TGTCAGGCCCCGGGGCAGAGTACGGACTGTGAGAGAGGGGCTTCTTCAACGGCT	459
OY	567	TTGGGAATCCATCTCAGACGATGTGCTGAGCTGTCCAGGTGCGGGACGAAATGTTCCAG	626
Db	460	TCAGAAAAACACCTCAGACACTGCCCTCAGCTCTCCAAATGCGAAAGAAATGGGTGAC	519
OY	627	GTGAGATTTTGGCTTGTGTATGTGACCGGGGACCTGTGTGGGTGTGACAGGAAGAACAG	686
Db	520	GTGAGATCTCTTCTTTCACAGTGTGACCGGGACCGGTGTGGGTGTGACAGGAAGAACAG	579
OY	687	TACCGGGGAATCTGGGGGTGAAACTGGCTTCCGGTGTGTGAACCTGCAGCCTCTGTCCAAAT	746
Db	580	TACCGGGCAATTATGGAGTGAAGAAACCTTTTCCAGTCTTCAATTTGACGCTGTCTCAAT	639
OY	747	GGCAAGAGGAATATCCCTGCCAGGAGAGACAGACACCATTTGCACTTGCATATGGGC	806
Db	640	GGAGCCGTGACCTTCTCTGCGAGGAGAAACGAACACCGTGTGACCTGCATTCAGGT	699
OY	807	TTCTTTCTTAAAGGCGCCAGTGCATCTCTGTCACTGATTTGTAAAGAA---CAAGAGTGC	863
Db	700	TTCTTTCTTAAAGAAAGAGAGTGTGTCTCTGTACTTAATCTGTAAAGAAAGCCTGGAGTGC	759
OY	864	GAGAAGTATGTGCCAACCCGACCTTCAACTGTGTAAAGACTCTCAGAGCCAGGCACTACAC	923
Db	760	ACGAAGTGTGTCTACCCCAATGTGAATGTAAAGGCACTGAGAGACTCAGGCACTACAC	819
OY	924	GTACTATTACCCCTGTGATGTCTTGGGGCTTGTGCTGAGCACTCTTGACCTCTGTGTGC	983
Db	820	GTGCTGTGGCCCTGTGTCTTTTCTTTGGTCTTTTGCTTTTATCTCTCTCTTCAATGGT	879
OY	984	TTAGCATGTCCGTACACGGGTGTGAAGCCCAAGCTCTACCTGCATCTTTGGGGGCAGTGG	1043
Db	880	TTAATGTATCTCTACCAACGGGTGAAGTCTCAAGCTCTCATTTGTTGTGGGAAATCG	939
OY	1044	ACTCTGTAAAGAGGGGAGCGACAGAA-----CTCCGTGTCCGGGGCCCAAGCTTC	1094
Db	940	ACACTGTAAAGAGGGGAGGAGCTTAAAGGAATCTACTTAAGCCCTGTGCCCCCAACCA	999
OY	1095	AACCCACACCAACCATCTGCTTCAAGTGCACCCCAAGTGTCCAGTCTGTCTCAATTC	1154
Db	1000	AGCTTCAATCCCACTCCAGAGCTTCAACCCCAACCTGGGCTTCAAGTCCCGTGGCAATTCC	1055
OY	1155	CCTTACATCTCTGTGAACGGGTCCAACTTGGGAG-----CGTGGCACTTCCCTCC	1205
Db	1060	ACCTTCACTTCAAGTCAACCTAATACCCCGGTGACTGTCCCAATTTTGGGCTCCCGC	1119
OY	1206	AGCGAGACGGCCCGGACCCCATCTTAAAGGCTGGCCCATCTTCCGGGCGCTCCGACTCC	1265
Db	1120	AGAGGGGTGACACCACTTATCAGGGGGCTGACCCCAATCT-----TTCTG	1166
OY	1266	ACCCACCTCTGTACCCCGGGGCTTCCGGGCTTCACCACTCTGTATCCCGGGGCTTCGG	1329

Db 1161 -----TGCAACAGCCCTC 1173

Qy 1326 GCCTTCACCCACCTCTGCAACCCAGTTACAGAAAGGGAAGCAGACGCCCCAGAGCCCC 1385

Db 1174 GCCTTCACCCCACTCCCAACCCCTTCAGAAAGGGAAGACAGCGCCACAA---ACCA 1230

Qy 1386 GATACGCTCGCGATGCCGACCCCGGCAACCTGTACCGGTGTGAACGCGTGCCTCG 1445

Db 1211 CAGAGCCTAGACACTGTATGACCCCGGCAAGCTGTACCCGTGTGGAGAAAGTCCCTCG 1290

Qy 1446 TCGGCTCGAAGAGAGTTGTATCGCCGCGCTGGAACTGAGCCAGACAGATCTGAGCCGCTG 1505

Db 1291 TTGGCTCGAAGAGAAATTCGTCCGCGCTCTAGGCTGAGCGACCAAGAACTGAATCGGCTG 1350

Qy 1506 GAGCTCGAGAAACGAGGCGCACCTCGCGAGGCGCAGATACAGCATCTCGCGGCTCGCGG 1565

Db 1351 GAGCTCGAAGAACGAGCGCGCTGCTCGCGAGGCGGCAATACAGCATGCTGTGGCACTTGAAGG 1410

Qy 1566 CGGCGCAACGCGCGCGCGAGGCCACGCTGAGCTGTGGGCGCGCTGTCAAGGACATG 1625

Db 1411 CGGCGCAACGCGCGCGCGAGGCCCAAGCTGTGAAGACGCGTGTCCGAGCATG 1470

Qy 1626 GACCTGCTGGGTTTGCCTGGAAGAAACATAGAGAGAGCGCTGGGTGGCGCGCCGCTTGGC 1685

Db 1471 GACCTGCTGGGCTTGCCTGGAAGAAACATGAGAGAGCGCTTTGCGGCCCGCGCTTCCG 1530

Qy 1686 TCGGAGCCCGGCTTCTCTGGTGAAGCCCGGCGCTTCG 1724

Db 1531 CCGCGCCCAAGTCTTCTCAAGTGAAGGCTGGGACCCCTTCG 1569

XX	AAH48859 standard; DNA; 2111 BP.
XX	AAH48859;
DT	12-NOV-2001 (first entry)
DE	Human TNFBP-associated DNA #1.
XX	TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW	insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW	antiprotocol; treatment; meningococcal sepsis; cerebral malaria;
XX	autoimmune glomerulonephritis; ds.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	187..1554
CDS	/tag= a
FT	/product= "TNBP-associated protein"
FT	187..270
sig_peptide	/tag= b
FT	271..1551
mat_peptide	/tag= c
EP1132471-A2.	
PD	12-SEP-2001.
PF	31-AUG-1990; 2001EP-0108117.
PR	12-SEP-1989; 89CH-0003319.
PR	08-MAR-1990; 90CH-0000746.
PR	20-APR-1990; 90CH-0001347.
PR	31-APR-1990; 90BP-0116707.
PR	31-AUG-1990; 99BP-0100703.
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.
X1	Brockhaus W, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

PI Schlaeger E;
 XX WPI: 2001-559312/63.
 DR P-PSDB; AAB86817.
 XX
 PT New homogeneous, insoluble proteins that bind tumor necrosis factor
 (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
 XX
 PS Claim 4a; Fig 1; 26pp; German.
 XX
 CC This invention describes novel insoluble proteins (I), also their
 CC (in) soluble fragments and pharmaceutically acceptable salts, able to bind
 CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
 CC invention have antiinflammatory, immunosuppressive, antibacterial,
 CC antiprotoccol activity. (I), and related recombinant proteins, are used
 CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
 CC sepsis; development of autoimmune glomerulonephritis and cerebral
 CC malaria. Also (I), or antibodies specific for them, are used for
 CC diagnostic determination of TNF in body fluids, for affinity purification
 CC of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
 CC human TNF binding protein described in the method of the invention.
 XX
 SQ Sequence 2111 BP; 447 A; 627 C; 587 G; 450 T; 0 other;
 Query Match 29.7%; Score 725.8; DB 22; Length 2111;
 Best Local Similarity 70.0%; Pred. No. 5e-139;
 Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;
 QY 148 TGTCCCGCCCGCAGCTTCAACCTTCACTCCCGACCGGAGCCCGGCTCCATGAGCA 207
 DB 41 TCTCTATGCCGATCTCAACCTTCACTCCCGACCGGAGCCCGGCTCCATGAGCA 100
 QY 208 TACCGGAGACCGGTGTGCTGCTCACTGCGGAGCCCGCCTGCTCC-CAGCCTGATGAG 266
 DB 101 AGACCGAGTCCCGGAGAGCCCGACGACCTGCGGAGCCCGCCTGAGCCAAATGG 160
 QY 267 GGATTGAGAGGCGCACAGTGGCCGACATGAGGCTCCCGACCGGCTGCTGCTGCTG 326
 DB 161 GGAATGAGAGGCGCACAGTGGCTGCTGAG-CATGAGGCTCTTCCACCGGCTGCTGCTG 219
 QY 327 CCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 386
 DB 220 CCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 279
 QY 387 CTTCAACCCCGGAGCCTGAGAGAGAGAGAGTCCCTGCTCCCAAGAAATATATACAC 446
 DB 280 CCTCACTTAAAGGAGAGAGAGAGAGATAGTGTGCTCCCAAGAAATATATATACAC 339
 QY 447 CCGGAAATATAGACATTTGCTGACCAAGTCCCAAGAGTATCTGTATCAATGAC 506
 DB 340 CTTCAAAATATATTTGATTTGCTGTACCAAGTCCCAAGAGTATCTGTATCAATGAC 399
 QY 507 TGTCCGGGTCCAGGGCGAGACAGGAGCTGAGGGTGTGCTCCCTGACCTTACATGACC 566
 DB 400 TGTCCAGGCGCGGAGAGATGAGAGCTGAGGAGGTGTGAGAGCGGCTCTTACCGCT 459
 QY 567 TTGAGAGACCATCTCAGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626
 DB 460 TCAGAAACACCTCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
 QY 627 GTGAGATTTTGGCTTGT 686
 DB 520 GTGAGATTTTGT 579
 QY 687 TACCGGAGATCTAGGGGTGAAATGCTTCCGGGTGTGAACTGACGCTTGTGCCAAT 746
 DB 580 TACCGGAGATTTAGAGTGAATACCTTTTCCAGTGTCTTCAATTCAGGCTTGTGCTCAAT 639
 QY 747 GGCACAGTGAATATCTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 806
 DB 640 GGCACAGTGAATATCTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699
 QY 807 TTTCTTTTAAGGCGGCAAGTGCATCTCTGTGTATGTAAGAA---CAAGAGTGC 863

DB 700 TTTCTTTAAGAGAAACGAGTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 759
 QY 864 GAGAGTATGTCCACACCCGACCTTCAACTGTAAAGCTTCGAGACCCAGGACATACA 923
 DB 760 ACGAGTGTGTCTTACCCGAGATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
 QY 924 GTACTATTACCCCGT 983
 DB 820 GTGCTGTGTGCCCCGT 879
 QY 984 TTACAGT 1043
 DB 880 TTAATGTATGT 939
 QY 1044 ACTGT 1094
 DB 940 ACACCTTAAAG 999
 QY 1095 AACCCACACACACATCTGT 1154
 DB 1000 AGCTTGT 1059
 QY 1155 CTTTACATCTGT 1205
 DB 1060 ACCTTGT 1119
 QY 1206 AGGAG 1265
 DB 1120 AGAGAGT 1160
 QY 1266 ACCCACTGT 1325
 DB 1161 -----TGGAGAGCCCTC 1173
 QY 1326 GCTTCAACCACTGT 1385
 DB 1174 GCTTCAACCACTGT 1230
 QY 1386 GATAGCTGT 1445
 DB 1231 CAGAGCTTACACACTGT 1290
 QY 1446 TCGGCTGT 1505
 DB 1291 TTGGGCTGT 1350
 QY 1506 GAGCTGT 1565
 DB 1351 GAGCTGT 1410
 QY 1566 CGGCGGAG 1625
 DB 1411 CGGCGGAG 1470
 QY 1626 GACCTGT 1685
 DB 1471 GACCTGT 1530
 QY 1686 TCGGAGCCCGGCTTGT 1724
 DB 1531 CCGCGGCGGAGT 1569
 RESULT 9
 ID ABR84039 standard; cDNA; 2111 BP.
 XX ABR84039;
 AC
 XX
 XX
 DT 14-AUG-2002 (first entry)
 XX
 DE Human cDNA differentially expressed in granulocytic cells #610.

Human; ss: granulocytic cell; DNA chip; bacterial infection;
viral infection; parasitic infection; protozoal infection;
fungal infection; sterile inflammatory disease; psoriasis;
rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
cardiac reperfusion injury; renal reperfusion injury; ARDS;
adult respiratory distress syndrome; inflammatory bowel disease;
Crohn's disease; ulcerative colitis; periodontal disease;
granulocyte activation; chronic inflammation; allergy.

Homo sapiens.

WO200228999-A2.

11-APR-2002.

03-OCT-2001; 2001WO-US30821.

03-OCT-2000; 2000US-237189P.

(GENE-) GENE LOGIC INC.

Beazer-Barclay Y, Weiseman SM, Yamaga S, Vockley J;

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression
of genes associated with granulocyte activation, which serves as
diagnostic markers that is useful for monitoring disease states and
drug toxicity.

Claim 1, SEQ ID No 610; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation
(GCA), by detecting the level of expression of gene(s) (Gs) identified by
DNA chip analysis as given in the specification, and comparing
the expression level to an expression level in an unactivated
GC, where differential expression of Gs is indicative of GCA.
Also included are modulating (M2) Gs by contacting GC with an agent
that alters the expression of at least one gene in Gs; (2) screening (M3)
for an agent capable of modulating GCA or an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease using the
gene expression profile; (3) detecting (M4) an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease, by detecting the
level of expression in a sample of the tissue of gene(s) from Gs, where
the level of expression of the gene is indicative of inflammation;
(4) treating (M5) an inflammation (especially chronic) or in a tissue,
an allergic response in a subject, exposure of a subject to a pathogen
or sterile inflammatory disease, by contacting a tissue having
inflammation with an agent that modulates the expression of gene(s)
from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
modulating GCA; M3 is useful for screening an agent capable of modulating
GCA preferably in an inflammation in a tissue; M4 is useful for
detecting an inflammation (especially chronic) in a tissue, an allergic
response in a subject, exposure of a subject to a pathogen or sterile
inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
reperfusion injury, ARDS, adult respiratory distress syndrome,
inflammatory bowel disease, Crohn's disease, ulcerative colitis,
periodontal disease; also bacterial infection, viral infection,
parasitic infection, protozoal infection, fungal infection and M5 is
useful for treating one of the above conditions. The present
invention represents a gene differentially expressed in granulocytes.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
ftp.wipo.int/pub/published_pat_sequences.

Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;

Query Match 29.7%; Score 725.8; DB 24; Length 2111;

Best Local Similarity 70.0%; Pred. No. 5e-139;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

Qy	148	TGTCCTCCGCGCCGATCTCAACCTCCCACTCCCGCAACCCGAGCGCCGGGCTCCATCGGCA	207
Db	41	TCTTATGCGCCGATCTCAACCTCCCACTCCCGCAACCCGAGCATTTGGAAGTCTCGAC	100
Qy	208	TACCGGAGGACCGGTGTGTCTGTCATCTGCGGGGCGCCACTGCGC-CAGCGCTGATGAG	266
Db	101	AGACCGAGTCCCGGAGAGCCCGACACTGCGCGCACTGCGCGCACTGCGCGCAATGAG	160
Qy	267	GGATTGAGAGCGCACAGCTGCGCGGAGAGAGTCCCTGCGCCCAAGGAAATATATACAC	326
Db	161	GGAAGTGAAGGCGCATGACTGCTGCG-CATGGGCTCTCCACCGTGCCTGACTGCTG	219
Qy	327	CCACTGCTGCTTCCAGCTCTGTGGCAGATGTGTATACCCCGAGGGGTTGAGGGGCTGTC	386
Db	220	CCGCTGTGTCTCCGAGGCTGTGTGGTGAATATACCTCAGGGGTTATTTGAGCTGTC	279
Qy	387	CCGACCCCGGGGAGCTGAGAGAGAGAGAGTCCCTGTCCCAAGGAAATATATACAC	446
Db	280	CCTACCTAGGGGAGAGAGAGAGAGATGTGTGTCTCCCAAGGAAATATATACAC	339
Qy	447	CCGCAAAATAGCACCATTTGTGACCAAGTCCCAAAAGTACTTATCTGTACATGAC	506
Db	340	CCTCAAAATATATGATTTGTGTACCAAGTCCCAAAAGTACTTATCTGTACATGAC	399
Qy	507	TGTCGGGCTGAGGCGGAGACAGGACTGCAAGGTGTGTGCTCCCTGCACTTACATGCC	566
Db	400	TGTCGAGGCGCGGGGAGAGATCGGACTGCAAGGAGTGTAGAGCGGCTCTTACCGCT	459
Qy	567	TTGAGAGACCATCTCAGACGATGCTGAGCTGCTCCAGTGCCTGGAGCAATATTCAC	626
Db	460	TCAGAAAACCATCTCAGACGATGCTGAGCTGCTCCAAATGCGAAGAAATGGTGC	519
Qy	627	GTGAGATTTGCGCTTGTGTAGTGAACCGGAGACCTGTGTGCGGCTCGAGGAACAC	686
Db	520	GTGAGATTTGCTTGTGTGACAGTGAACCGGAGACCTGTGTGCGGCTCGAGGAACAC	579
Qy	687	TACCGGGAATCTGGGAGTGAACCTGCTCCCGTGTGTGAACCTGACCTGTGCCAT	746
Db	580	TACCGGGAATTTGAGTGAACCTTCTTCCAGTCTCAATGACCTGTGCTCCAT	639
Qy	747	GGCAGAGTAATATCCCTGCGCAGAGAGACAGACCATCTGCACTGCGCATATGGGC	806
Db	640	GGACACGTGACCTCTCTGCGCAGAGAGACAGACCATCTGCACTGCGCATATGGGC	699
Qy	807	TTCTTTTCTTAAAGGCGCCAGTGCATCTCTGTATGATTTGAAGAA--CAAGAGTGC	863
Db	700	TTCTTTTCTTAAAGAGAAAGAGTGTGTCTCTGTATGATTTGAAGAAAGCTGAGTGC	759
Qy	864	GAGAGATATATCCACCCGACCTTCAACCTGTAAAGACTCTGAGGCCGAGCACTACA	923
Db	760	ACGAGATTTGCGCTTACCCAGATTTGAAGATTTAAAGGCACTGAGGACTGAGCA	819
Qy	924	GTACTATTAACCCCTGTGATTTGTCTGCGGCTTGTGCGGATCTTGTGCTGCTG	983
Db	820	GTGCTGTGCGGCTGTGATTTTCTTGTGTCTTGTGCTTATATCCCTTTCATTTGCT	879
Qy	984	TTAGCATGTGCTTACCAAGCGGTGAAGCCCAAGCTTACTTCACTATTTTGGGCAAGTG	1043
Db	880	TTAATGATGCTTACCAAGCGGTGAAGTCAAGCTTACTTCACTATTTTGGGCAAGTG	939
Qy	1044	ACTCTGTAAAGAGGGGAGCCGAGAA-----CTCCGTGTCCCGGCGCCGAGGCTTC	1094
Db	940	ACACTGTAAAGAGGGGAGCCGAGAACTACTTAAAGCCCTTGGGCGCCCAACCCA	999
Qy	1095	AAACCCACCAACCATCTGCTGAGCTCCAGCCCAAGTTCAGTCTCTTCCATTTCC	1154
Db	1000	AGCTTCACTCCCATCTCAGAGCTTACCCCGACCTGAGGCTTCAATCCGATGCCAGTTC	1059
Qy	1155	CTTACATCTCTGTGACGGTTCCAACTTGGAG-----CGTGCATCTTCCCTCC	1205

Db 1060 ACCTTCACTCCAGTCCACTATACCCCGGTAATCTCCCACTTTGGCGCTCCCGC 1119
 QY 1206 AGCGAGACGCGCCCGCCCATCTAAAGGCTGAGCCCATCTCCCGGCGCTCCGCGCTCC 1265
 Db 1120 AGAGAGGTGGACCAACCTATCAGGGGAGCTGACCCCATCTC----- 1160
 QY 1266 ACCACCTCTTATCCCGGGGCTCCCGGCTCCACCCACTCTGTATCCCGGGGCTCCG 1325
 Db 1161 -----TGCGACAGCCCTC 1173
 QY 1326 GCTTCAACCCACCTCTGCAACCCAGTTGAGAAAGTGGAAAGGCGAGCGCCCGCCCGC 1385
 Db 1174 GCTTCCAGCCCATCTCCCAACCCCTTGAAGAGTGGAGAGAGGAGCCACAGCA---AGCCA 1230
 QY 1386 GATCAGCTGCGGATGCGGACCCCGGACCCCTGTATACGCGGTGTGAGACGCGTCCCGC 1445
 Db 1231 CAGAGCCCTAGACACTGATGACCCCGCGACGCTGTATCCCGGTGTGAGAAAGTCCCGC 1290
 QY 1446 TCGGCTGGAAGAGTGTGTGCGCGGCTGGGACTGAGCCGACAGAGATGAGCGGCTG 1505
 Db 1291 TTGGGCTGGAAGAAATTCGTGCGCGGCTTACGCGCTGAGCCGACAGAGATGATCGGCTG 1350
 QY 1506 GAGCTGAGAGACGAGCGCCGCACTGCGCGAGGCGAGATGACAGATGCTGGCGGCTCCGCG 1565
 Db 1351 GAGCTGAGAGACGAGCGCGCTGCTGCGAGGCGCAATACAGCATGCTGGAGCTTGAAG 1410
 QY 1566 CGGCGCAACGCGCGCGCGGAGGCGCAAGCTGAGCTGCGCGCTGCTGAGGAGATG 1625
 Db 1411 CGGCGCAACGCGCGCGCGGAGGCGCAAGCTGAGCTGCGCGCTGCTGAGGAGATG 1470
 QY 1626 GACCTGCTGGGTTCCTCTGAGAAACATAGAGAGGCGCTGGGTGGCGCGCGCTGCGC 1685
 Db 1471 GACCTGCTGGGTTCCTCTGAGAGACATGAGAGAGGCGCTGGGTGGCGCGCGCTGCGC 1530
 QY 1686 TCCGAGCCCGCGCTTCTCTGCTGAGAGCCCGCGCCCTCCG 1724
 Db 1531 CCGCGCGCGAGCTTCTCAAGTGAAGGCTGGCGCCCTGCG 1569
 RESULT 10
 ID ABR95862 standard; DNA; 2111 BP.
 XX ABR95862
 AC ABR95862;
 DT 13-AUG-2002 (first entry)
 XX Gene #2360 used to diagnose liver cancer.
 DE Gene, liver cancer; dr; hepatocellular carcinoma; hepatotropic;
 KM metastatic liver tumour; cytostatic; expression profile; disease state;
 XX disease progression; drug toxicity; drug efficacy; drug metabolism.
 OS Homo sapiens.
 XX NO200229103-A2.
 PN 11-APR-2002.
 PD 02-OCT-2001; 2001WO-US30589.
 PF 02-OCT-2000; 2000US-237054P.
 PR (GENE-) GENE LOGIC INC.
 PA Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 PI WPI; 2002-426119/45.
 DR
 XX Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample

XX Claim 1; SEQ ID NO 2360; 298bp; English.
 PS
 CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumour in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABR93503-ABR97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wipo.int/pub/published_pct_sequences.
 SQ

Query Match 29.7%; Score 725.8; DB 24; Length 2111;
 Best Local Similarity 70.0%; Pred. No. 5e-139;
 Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

QY 148 TGTCCCGCCCGCCAGTCTCAACCTCCACTCCCGAGCGCGGCGCTCCACTGCGCA 207
 Db 41 TCTCTATGCCCGAGTCTCAACCTCAACTGTCAACCCCAAGGCACTTGGAGCTCTGAGC 100
 QY 208 TACGCGAGACCGGTGTCTGTCACTGTGCGGCGCGCACTGCC-CAGCCCTGATGAG 266
 Db 101 AGACCGAGTCCCGGAGAGCCCGCAGCACTGCGCTGCAACATGCTCCGAGCCCAATGAG 160
 QY 267 GGAATTGAGAGGCGCAAGCTGCGCGGAGATGAGGCGCTCCCAAGCTGCGCTGCGCTG 326
 Db 161 GGAATTGAGAGGCGCAAGCTGCGCGGAGATGAGGCGCTCCCAAGCTGCGCTGCGCTG 219
 QY 327 CCACTGATGCTTCCAGCTCTGAGTGTGAGATGTATACCCCGAGGCGCTTCAAGGCGCTGTC 386
 Db 220 CGCTGTGTGCTCTGAGAGCTGTGTGAGGAGATATACCTCCAGGCGTTATGAGACTGCTG 279
 QY 387 CTTCAACCCCGGAGACTGAGAGAGAGAGAGAGTCCCTGTCTCCCAAGAAATATATACAC 446
 Db 280 CTTCAACCTAGGAGAGAGAGAGAGAGATGATGTGTCTCCCAAGAAATATATATACAC 339
 QY 447 CCGCAAAATATAGACCAATTTGCTGCAAGTGTCCCAAGATGCAATCTGTATCAATGAC 506
 Db 340 CTTCAAAATATATTTGATTTGCTGTACCAAGTGTCCCAAGATGCAATCTGTATCAATGAC 399
 QY 507 TGTCCCGGCTCCAGGCGGAGACAGAGCTCAGAGGTGTGCGCCCTGCGACCTTACACTGCG 566
 Db 400 TGTCCAGGCGCGGCGGAGATACAGACTGCAAGGATGTGAAGCGGCTCTTCAACCGCT 459
 QY 567 TTGGAGAACCATCTCAAGCAATGCTGACTGCTCCAGGTGTCGAGACGAAATGTTTCAG 626
 Db 460 TCAGAAACCACTCAAGACATGCTGCTCACTCCAAATGTCGAAAGAAATGAGGTGAG 519
 QY 627 GTGAGATTTGCGCTTGTGTATGAGACCGGAGACATGTGTGGCGGTGCGAGAAACGAG 686
 Db 520 GTGAGATCTCTTGTGACAGTGTGACCGGAGACATGTTGTGTGTGCGAGAAACGAG 579
 QY 687 TACCGGAAATCTGAGGTGAAATGAGCTTCCGGTGTCTGACATGAGCTCTGTCTCCCAAT 746
 Db 580 TACCGGCAATTTGAGGTGAAACCTTTTCAGTGTCTCAATTTGAGCTCTGTCTCCCAAT 639
 QY 747 GGCACAGTGAATATCCCTGCGCAGAGAGACAGACCATTTGCCACTGCTCATATGAGGC 806
 Db 640 GGCACCGTACACTCTCTGCGCAGAGAGAAACAGAACCATGCTGCGCATCAGGT 699
 QY 807 TTTCTTCTTAAAGGCGCAAGTGCATCTCTGCTGATGATGTAAGA---CAAGAGATGC 863
 Db 700 TTTCTTCTTAAAGGAAACGAGTGTGTCTCTGATGATGTAAGAAGAAAGCTGAGATGC 759

QY 864 GAGAGTTATGTCACACCGACCTTCACTGGTAAAGACTCTGACAGCCAGCACTACA 923
 DB 760 ACGAAGTTGTGTACCCCAATGATGATGAAAGGACCTGAGGACCTCAGGACACACA 819
 QY 924 GTACTATTACCCCTGTGATGTTGCTTCGGGCTTTTGCCTGGACATCTTGCCTGTCTC 983
 DB 820 GTGCTGTGCCCCCTGTGATTTCTTTGGTCTTTTGTCTTTTATCCCTCTCTTCAATGCT 879
 QY 984 TTAGCATGCTGTTACAGAGGTTGAGGCCCAAGCTTACTTCATCTTTGGGGCAGTCCG 1043
 DB 880 TTAATGTATCGCTACCAACGGTGAAGTCCAAAGCTTACTCTCATTTGTTGGGAAATCG 939
 QY 1044 ACTCTGTAAAGAGGGGAGGACCAAGAA-----CTCCGTGTGCTCCGAGCCCAAGCTTC 1094
 DB 940 ACACCTGAAAAGAGGGGAGCTTGAAGAACTACTACTAAAGCCCTTGGCCCAACCA 999
 QY 1095 AACCCACACACCAACCATCTGTTCACTTCAACCCCAAGTTCCAGTCTCTCAATGCC 1154
 DB 1000 AGCTTCAGTCCCACTCAGAGGCTTCAACCCCAACCTTGGGGCTTCAAGTCCGATGCC 1059
 QY 1155 CTTTACATCTCTGTGACCGGTCACACTTCCGAG-----CCGTGCATCTCTCTCC 1205
 DB 1060 ACCTTACCTCCAGCTCCACCTATACCCCGGTGACTGTCCCACTTGGCCGCTCCCGC 1119
 QY 1206 AGCGAGAGGGCCCGCCCATTAAGGCTGCCCCATCTCCCGGGGCTCCGGCCTCC 1265
 DB 1120 AAGAGGTTGGACCAACCTTATAGGGGGCTGACCCCATCT----- 1160
 QY 1266 ACCCACTCTGTATCCCGGGGCTCCGCTCCACCACTCTGTATCCCGGGGCTCCG 1325
 DB 1161 -----TCCGACACCCCTC 1173
 QY 1326 GCCTTCACACCACTCTGACACCCCAAGTTCAAGATGAGGAAAGCCCGCCAGCCGCC 1385
 DB 1174 GCCTCCGACCCCATCCCAACCCCTTCAAGATGAGGAAAGCCCGCCACA--AGCCA 1230
 QY 1386 GATCAGCTGCGGATGCGGACCCCGGACCTCTGTACGCGGATGAGGACGCGCTGCCCG 1445
 DB 1231 CAGAGCTTGAACATGATATACCCCGGACGCTGTACGCGCTGTGAGAGACATGCTCCCG 1290
 QY 1446 TCGCGCTGGAAGAGTTGTTGCGGCGGCTGAGGACTGAGCGACAGATTCAGGCGCTG 1505
 DB 1291 TTGCGCTGGAAGAAATTGTCGCGGCGCTGAGGCGACAGAGATTCATCGGCTG 1350
 QY 1506 GAGCTGGAAGAGCGGCGGCACTGCGCGGAGCGGCACTGATGATGCTGCGGCTGCGG 1565
 DB 1351 GAGCTGCAAAAGCGGCGCTGCTGCGCGGAGCGGCAATACGATGTGCGGACTGGAAG 1410
 QY 1566 CGGCGACGCGCGGCGGAGGACAGCTGAGAGCTGAGGCGGCTGCTCAAGGACATG 1625
 DB 1411 CGGCGACGCGCGGCGGAGGCGAGGCGAGCTGAGAGCTGAGAGCGCTGCTCCGCAATG 1470
 QY 1626 GACCTGCTGGTTGCTTGAAGAAACATAGAGAGCGCTGAGCGCGCGGCTGCGG 1685
 DB 1471 GACCTGCTGGGCTGCTTGAAGGACATGAGAGAGCGCTTTGGGCGCGCGGCTGCGG 1530
 QY 1686 TCGAGACCGCGCTTCTTGTGTAAGCGCGCGCTCCG 1724
 DB 1531 CCGCGCGCCAGTCTTCTCAGATGAGGCTGCGCGCTGCG 1569

XX OS Homo sapiens.
 FN US6007995-A.
 XX PD 28-DEC-1999.
 XX PP 26-JUN-1998; 98US-0106038.
 XX FR 26-JUN-1998; 98US-0106038.
 PA (ISIS-) ISIS PHARM INC.
 PI Baker BF, Cowsebert LM;
 DR WPI; 2000-105333/09.
 XX PT Antisense inhibition of tumor necrosis factor type 1 expression for
 PT diagnosis, treatment and prevention of disease, particularly tumors
 XX
 PS Example 10; Columns 33-36; 34pp; English.
 CC The invention provides antisense compounds targeted to human tumour
 CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
 CC can be used in a method of inhibiting the expression of TNFR1 human cells
 CC or tissues. The antisense compounds specifically hybridize with one or
 CC more nucleic acids encoding TNFR1, ultimately modulating the function of nucleic
 CC acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1
 CC produced. The antisense compounds and method are useful as research
 CC reagents and diagnostics, and in the treatment and prophylaxis of
 CC infection, inflammation or tumour formation. The present sequence
 CC represents the nucleotide sequence of human TNFR1 (Genbank Accn No:
 CC X55313).
 XX
 SQ Sequence 2161 bp; 459 A; 642 C; 604 G; 456 T; 0 other;
 Query Match 29.7%; Score 725.8; DB 21; Length 2161;
 Best Local Similarity 70.0%; Pred. No. 5e-139;
 Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;
 QY 148 TGTCCCGCGCCAGTCTCAACCTTCCACTCCGACCCGAGCGCCGCTTCACCTGGCA 207
 DB 110 TCTCTATGCCGAGTCTCAACCTTCAACTGTCACCCCAAGCACTTGGGACGTCTGGAC 169
 QY 208 TACCGAGGAACCGTGTGTCTCACTGTCGCGGCGCCGCACTGCC--CAGCCCTGATGGG 266
 DB 170 AGACCGAGTCCCGGAGAGCCCAAGCACTGCGCTGCCACACTGTGAGCCCAAAATGGG 229
 QY 267 GGATTGAGAGGCAACAGCTGCGCGGACATGGGCTCCCACTGAGCTGAGCTGCTGCTG 326
 DB 220 GAGTGAAGAGCCATAGCTGTCTGG--CATGGGCTTCTCAACCGTGGCTGAGCTGTGCTG 288
 QY 327 CCACGTGTGCTTCCAGCTCTGTGGCGAGATGTATACCCCGAGGAGTTACAGGGCTGCTC 386
 DB 289 CCGCTGTGTCTCTGAGAGCTGTGTGGGAAATATACCTTCAGGGAGTTATGACTGCTC 348
 QY 387 CCTCACCCCGGGGACCTGAGAGAGAGAGTCCCTGTCCCAAGGAAATATTAACAC 446
 DB 349 CCTCACCTAGGAGAGAGAGAGAGATGTGTGTCCCAAGGAAATATATTCAC 408
 QY 447 CCGCAAAATAGCACCATTTGCTGACCAAGTGCACAAAGTACTATCTGTACAAATGAC 506
 DB 409 CCTCAAAATATTTGATTTGCTGTACCAAGTGCACAAAGTACTATCTGTACAAATGAC 468
 QY 507 TGTCCGGGTCAGAGGCGAGACAGGACTGCAAGGTGTGTGCTCCCTGACCTTACATGCC 566
 DB 469 TGTCCAGGCGCGGGGACAGATACGGACTGACAGGAGTGTGAGAGCGGCTCTTCAACCCCT 528
 QY 567 TTGGAAGACCATCTCAAGCATGTGCTGAGCTGCTCCAGAGTCCCGGAGAGAAATGTTCCAG 626
 DB 529 TCAGAAAACCACTCAAGCACTGCTTCAAGTGTCTTCAATGCCCAAGAAATGGGTAG 588-
 QY 627 GTGAGATTTGCGCTTGTGTAGTGAACGGGACACTGTGTGCGGCTGAGGAAAGAACGAG 686

RESULT 11
 AA248475 standard; DNA; 2161 BP.
 AA248475;
 31-MAR-2000 (first entry)
 Human tumour necrosis factor receptor (TNFR1) nucleotide sequence.
 Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
 inflammation; tumour formation; TNFR1; anticancer; ds.

Db	589	GTGGAGATCTTCTTTCGACAGTGGACCGGGACACCGGTGTGGCTGACGGAAAGAACG	648
OY	687	TACCGGGAATATCTGGGGTGAATCTGGCTTCGGGTCTGAACTGCACCTCTGTCCAAAT	746
Db	649	TACCGGCAATATATGGAGTGAATACTTTTTCAGTGTCTTCAATTCGACGCTGTGCTCAAT	708
OY	747	GGCAACAGTGAATATCCCTGTGCAGAGAGAGAGACACATCTTCCACTGTGCATATGGCC	806
Db	709	GGGACCGGTGACCTCTCCTGTGCAGAGAGAAACAGAACCGGTGTACCTGTGCATGACAGT	768
OY	807	TTCTTCTTAAAGGCGCCAAAGTCATCTCCGTGTATGATTTGTAAAGAA---CAAGAGTGC	863
Db	769	TTCTTTCTAAGAGAAAAGAGTGTGTCTCTCTGTAGTACTGTAAAGAAAAGCTTGAATGC	828
OY	864	GAGAAATTATGTCCAAACCCGACCTTCACTGTGTAAAGACTTTCAGAGACCCAGGCACTACA	923
Db	829	ACGAAGTTGTGCTTACCCCAATTGAGAAATGTAAAGGCACTGAGGACTGACGACACACA	888
OY	924	GTACTATTTACCCCTGTGTGATTTGTCTTGGGGCTTTTGCCTGGATCTCTTGCTGTGTCTC	983
Db	889	GTGTGTGTGTGCCCCGTGTGCTATTTCTTTGTGTGTGTGTGTGTGTATCCCTCTCTTCAATGGT	948
OY	984	TTAGCAATGTGCTTACACGGGGTGAAGCCAAAGCTTACTCATTCATTTTGGGGCAATGG	1043
Db	949	TTAATGTATGCTTACCAACGGGTGAAGTCCAAAGCTTACTCATTTGTTTGGGAAATTCG	1008
OY	1044	ACTCTGTAAAGAGGGGGAGCCAGAA-----CTCCTGTGCCGGCCCCAGGCTTC	1094
Db	1009	ACACTGTAAAGAGGGGGAGCTTGAAGAACTACTACTAAGCCCCGTGTGGCCCCAAATCCA	1068
OY	1095	AACCCACCAACCAATCTGCTTACAGTCCACCCCAAGTTCAGTCTGTCTCATTTCCC	1154
Db	1069	AGCTTCAGTCCCACTCCAGGCTTCAACCCCACTTGGGGCTTCAAGTCCCGTGTCCAGATTCC	1128
OY	1155	CTTACATCTCTGTGACCGGTGCCAATTTGAG-----CGTGTGATCTTCCCTCC	1205
Db	1129	ACCTTCACTCAAGCTCCACTATATACCCCGGTGACTGTGCCAACTTTTGGCTCTCCCGC	1188
OY	1206	AGCAGACAGGCCCCGCCCATCTTAAAGGCTTGGCCCCCATCTCCAGGGACTCCGAGCTCC	1265
Db	1189	AGAAAGGTGGACCAACCTTATCAGAGGGGCTTAACTCCATCT-----	1229
OY	1266	ACCCACCTCTGPAACCCCGGGGCTTCGGGCTTCACCACTCTGTATCCCGGGGCTTCG	1325
Db	1230	-----TGGACAGCCCTTC	1242
OY	1326	GCTTCCACCCACTCTGTGACCCCACTTGAAGGTGGAAAGCCAGGCCCCCAAGGCCCCC	1385
Db	1243	GCTTCCGACCCCATCTCCCAACCCCTTTCAGAAAGTGGAGGACAGGCCCAACA---AGCA	1299
OY	1386	GATCAGCTCGCGAGATGCCGACCCCGGCAACCTGTATACGGGGTGTGGAGACGGGTGCCCGG	1445
Db	1300	CAGAGCTTATGACATGTATGACCCCGGCAAGCTGTATGCCGTGTGTGAAGAACTGTGCCCG	1359
OY	1446	TCGGCGTGAAGAGATTGTGTGCGGCGCTGTGGACTTGAAGCGACAGAGATCGAGCGGCTG	1505
Db	1360	TTGGGCTGTGAAGGAATTCGTGCGGGGCTTAAAGGCTGACGACCAAGAGATGATGTGGGTG	1419
OY	1506	GAGCTGGAAGAACGGGCGGCCACTGTGGCGAGGCGCAGTACAGCATGTCTGGCGGCTTGGCGG	1565
Db	1420	GAGCTGCGAAGACGGGCGCTGCTGTGGCGAGGCGCAATACAGCATGTCTGGCACTGTGAGG	1479
OY	1566	CGGGGCAAGCGGCGCGCGAGAGGCAAGCTGAGAGCTGTGGGCGCGCGTCAAGGGAACATG	1625
Db	1480	CGGCGCAAGCGGCGCGGCGAGAGGCAAGCTGAGAGCTGTGGGACCGGTGTCTCGGACACATG	1539
OY	1626	GACCTGTCTGTGGTTGCTGTGAAGAAACATAGAGAGGCGCTGTGGTGGCGCGCCGCTCTGCG	1685
Db	1540	GACCTGTCTGTGGCTGTGTGAAGAACATGAGAGAGGCGCTTGTGGGCGCGCGCTCTCCG	1599
OY	1686	TTCCGAGCCCCGCTTCTCTGTGAAGCCCCCGCTTCG	1724

Db 1600 CCGGCGCCAGTCTTTCAGATGAGCTGGCGCCCTGCG 1638

RESULT 12

ID ABR04971 standard; DNA; 2161 BP.

XX ABR04971

AC ABR04971;

XX

XX

XX 11-OCT-2002 (first entry)

XX

DE Cytokine tumour necrosis factor (TNF) polynucleotide SEQ ID No 1.

XX

XX Antisense compound; tumour necrosis factor receptor 1; liver disease;

KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;

KW human; ds.

XX

OS Homo sapiens.

XX

XX MO200248168-A1.

XX

XX 20-JUN-2002.

XX

XX 22-OCT-2001; 2001WO-US51224.

XX

XX 24-OCT-2000; 2000US-0695451.

XX

XX (ISIS-) ISIS PHARM INC.

XX

PI Baker BF, Cowse LM, Zhang H, Dean NM;

PI WPI; 2002-583481/62.

DR P-PSDB; AAO22286.

XX

XX Novel antisense compound targeted to nucleic acid molecule encoding

PT tumor necrosis factor receptor 1 (TNFR1), useful for treating humans

PT having disease associated with TNFR1 e.g. hepatitis, liver injury,

PT liver cancer

XX

XX Example 10; Page 69-71; 121pp; English.

XX

XX The invention relates to an antisense compound 8 to 30 nucleotides in

CC length targeted to nucleic acid molecule encoding tumour necrosis factor

CC receptor 1 (TNFR1), where the antisense compound inhibits expression of

CC TNFR1. The antisense compound is useful for inhibiting the expression of

CC TNFR1 in cells or tissues. The antisense compound is also useful for

CC treating an animal (preferably human) having a disease or condition

CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver

CC injury) or a hyperproliferative disorder such as cancer, by inhibiting

CC the expression of TNFR1. The antisense compound is useful for

CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.

CC This polynucleotide sequence represents a human nucleic acid sequence

CC relating to the TNFR1 of the invention.

XX

XX Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;

XX

XX Query Match 29.7%; Score 725.8; DB 24; Length 2161;

XX Best Local Similarity 70.0%; Pred. No. 5e-139;

XX Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

XX

QY 148 TGTCCGCGCCCACTCAACCTCACTCCCGACCCGAGGCCGAGCTCACTGGACA 207

Db 110 TCTGTATGCGCCGAGTCTCAACCTCACTCAACCCCAAGCACTTGGAGAGTCTGGAC 169

QY 208 TACCGGAGGACCGGTGTTGCTGTCACTGTCGGGCGCCCACTGCC-CAGCCCTGATGGG 266

Db 170 AGACCGAGTCCCGGGAAGCCCAACCACTGCGCTGCACACTGCCCTGAGCCCAAAATGG 229

QY 267 GGATTTGAGAGGCCACAGCTGGCCGGAATGAGGCTCCCAACCGTGGCTGATGCTGCTG 326

Db 230 GGAATGAGAGGCCATAGCTGCTGG-CATGGGCTCTTCCACAGTGGCTGACTGCTGCTG 288

QY 327 CCACTGTGCTTCCAGTCTGTTGGCAGATGTGTACCCCGAGGAGGATTCAAGGAGCTGATC 386

CC combination of a death domain receptor ligand and a diterpenoid
 CC triepoxide. This method has cytostatic activity and works by blocking
 CC TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the
 CC invention may be used for treating tumours, particularly solid tumours,
 CC e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma
 CC also neurological malignancies, haematological malignancies, e.g.
 CC non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant
 CC cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma,
 CC lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia,
 CC bullous pemphigoid, discoid lupus erythematosus, lichen planus. The
 CC combination may be administered with other active agents, e.g. anti-
 CC metastatic, anti-tumour or anti-angiogenic agents. The potent synergy
 CC between the diterpenoids and the death domain ligands allows increased
 CC killing at equivalent or lower doses, and can sensitize otherwise
 CC resistant cells. This sequence represents the human tumour necrosis
 CC factor alpha receptor (TNF-R1) DNA. TNF-R1 is a death domain receptor
 CC used in the used method of the invention in combination with diterpenoid
 CC triepoxides to kill tumours by inducing apoptosis.

XX Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;

Query Match 29.7%; Score 725.8; DB 24; Length 2161;

Best Local Similarity 70.0%; Pred. No. 5e-139; Mismatches 387; Indels 92; Gaps 7;

Db 110 TCTCTATGCGCCGAGTCTCAACCTCACTGCTCACCCTGAGGCACTTGAGAGTCTCTGAC 169
 Qy 148 TGTCCCGCCCGCACTCTCAACCTCTCACTCCCGACCCGAGGCCCGGGCTTCCACTGAGCA 207
 Db 208 TACGCGAGGACCGCTGTGTCTCTCACTGTGCGGGCCGCTCACTGCCC-CAGGCTCTGATGGG 266
 Qy 170 AGACCGAGTCCCGGAGAGCCCGACACTGCGCTGACCACTGCTGAGGCCCAATGG 229
 Db 267 GGAATTGAGAGGCACTGAGCGGAGACATGAGGCTCCCGACCTGAGCTGCTGCTGCTG 326
 Qy 230 GGAATGAGAGGCACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
 Db 327 CCACTGTGTCTTCCAGCTCTGTGTGAGAGTGTACCCCGAGGGGCTTCAAGGGCTGCTG 386
 Qy 289 CCGCTGTGTCTTCCAGCTCTGTGTGAGAGTGTACCCCGAGGGGCTTCAAGGGCTGCTG 348
 Db 387 CCTCAACCCCGGAGCACTGAGAGAGAGAGAGTCCCTGTCCCAAGAGAAATATATACAC 446
 Qy 349 CCTCAACCTGAGGGGAGAGAGAGAGAGATGTGTGTCTCCCAAGAGAAATATATATAC 408
 Db 447 CCGGAAATATGACATTTGTGTGACCAAGTGCACAAAGGTACTATCTGTATATATGAC 506
 Qy 409 CCTCAAAATATTTGATTTGTGTGACCAAGTGCACAAAGGTACTATCTGTATATATGAC 468
 Db 507 TGTCCGGGTCCAGGGGAGAGACCGAGCTGAGGGTGTGTGCTCCCTGAGCACTTACATGAC 566
 Qy 469 TGTCCAGGCCCGGGGAGAGATGAGGAGTGTGAGAGCGGCTCTTCAACGGCT 528
 Db 567 TTGAGAAACCATCTCAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626
 Qy 529 TCGAAAAACCACTCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
 Db 627 GTGAGATTTTGGCTTGT 686
 Qy 589 GTGAGATTTTGGCTTGT 648
 Db 687 TACCGGAAATATGAGGGTGAATGAGCTTCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 746
 Qy 649 TACCGGCAATATGAGAGTGAATGAGCTTTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 708
 Db 747 GGCACAGTGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 806
 Qy 709 GGCACAGTGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
 Db 807 TTCTTTCTTAAAGGCGCAAGTGCATCTCCGTGATGATGTGTAGAA---CAAGAGTGC 863
 Qy 769 TTCTTTCTTAAAGGCGCAAGTGCATCTCCGTGATGATGTGTAGAAAGCTGAGAGTGC 828

Qy 864 GAGAAATTATGTCAACCCGACCTTCACTGTGTAAAGTCTCTGACAGCCAGGCACTTACA 923
 Db 829 ACCAAATTTGCTTACCCGACCTTCACTGTGTAAAGTCTCTGACAGCCAGGCACTTACA 888
 Qy 924 GTACTATTACCCGAGT 983
 Db 889 GTGCTGTGCTTGT 948
 Qy 984 TTGACATGTGCTTACAGCCGAGGAGAGCCAGCTTCACTGTGTGTGTGTGTGTGTGTGTGTGT 1043
 Db 949 TTATATGTATGCTTACAGAGGAGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1008
 Qy 1044 ACTCTGTGTAAAGAGGGGAGCCAGAA-----CTCTGTGTGTGTGTGTGTGTGTGTGTGT 1094
 Db 1009 ACACCTGAAAAAAGAGGGGAGCTTGAAGAACTACTTAAAGCCCTGTGTGTGTGTGTGTGTGT 1068
 Qy 1095 AACCCCAACCAACCACTGT 1154
 Db 1069 AGCTTCACTGT 1128
 Qy 1155 CTTTACATCTCTGT 1205
 Db 1129 ACCTTCACTGT 1188
 Qy 1206 AGCAGAGCGCCCGGCTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1265
 Db 1189 AGAGAGGT 1229
 Qy 1266 ACCCACTGT 1325
 Db 1230 -----TGT 1242
 Qy 1326 GCTTCAACCCGACCTGT 1385
 Db 1243 GCTTCAACCCGACCTGT 1299
 Qy 1386 GATCACTGT 1445
 Db 1300 CAGAGCTTGT 1359
 Qy 1446 TCGGCTGT 1505
 Db 1360 TTGT 1419
 Qy 1506 GAGGT 1565
 Db 1420 GAGGT 1479
 Qy 1566 CCGGCGACCG 1625
 Db 1480 CCGGCGACCG 1539
 Qy 1626 GACTGT 1685
 Db 1540 GACTGT 1599
 Qy 1686 TCCGAGCG 1724
 Db 1600 CCGGCG 1638

RESULT 14

ID AA090513 standard; DNA; 2175 BP.

AA090513:

19-JAN-1996 (first entry)

p55 TNF-R gene.

p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;

epidermal growth factor receptor; EGF-R; protease; inhibitor;

KM phorbol myristate acetate; PMA; 88.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 256..1623 /tag= a
 FT /product= p55 TNF-R
 FT mlec_signal 2143..2149 /tag= b
 FT /note= "possible poly-A signal"
 FT
 PN AU9475742-A.
 PD 04-MAY-1995.
 XX 11-OCT-1994; 94AU-0075742.
 XX 12-OCT-1993; 93IL-0107268.
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA
 PI Backin M, Brakebusch C, Varfolomeev E, Wallach D;
 DR WP1; 1995-194342/26.
 DR P-PSDB; AAR75084.
 XX
 PT New protease capable of cleaving soluble tumour necrosis factor
 PT (TNF) receptor - from cell-bound TNF- receptor, useful for
 PT antagonising deleterious effects of TNF.
 PS
 PS Disclosure; Fig 1; 40pp; English.
 XX
 CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
 CC Expression of this receptor is regulated by shedding of the
 CC extracellular receptor fragment. The p55 TNF-R can be shed in response
 CC to different inducing agents, e.g. phorbol myristate acetate (PMA),
 CC depending on cell type. The only region of the receptor whose structure
 CC affects the shedding response is the spacer region (see AAR75012) in the
 CC extracellular domain. This region is located close to a site of cleavage
 CC of the molecule, and links the Cys rich module to the transmembrane
 CC domain. The spacer region of the encoded protein was used to create the
 CC chimeras between human p55 TNF-R and murine epidermal growth factor
 CC receptor (EGF-R) that are represented by AAR75007-11. This spacer region
 CC was subjected to deletion mutations (AAR75013-25) and substitutions
 CC (AAR75026-47). Of the spacer region, the most important residues are
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
 CC important of these. The shedding of the receptor is independent of the
 CC side chain identity of these residues, with the exception of a limited
 CC dependence on the identity of Val 173. Mutations which alter the
 CC conformation of the protein adversely effect the shedding process. The
 CC mutations shown in AAR75013-47 were introduced in order to create an
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
 CC AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
 CC inhibitors can be used for enhancing TNF function.
 CC
 XX Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T; 0 other;
 SQ
 Query Match 29.7%; Score 725.4; DB 16; Length 2175;
 Best Local Similarity 69.6%; Pred. No. 6e-139;
 Matches 1128; Conservative 0; Mismatches 401; Indels 92; Gaps 7;

Db 230 GAAGTAGAGGCGCAGACGTGTCTGG-CATGGGCGCTTCCACGTCGCTGACCTGCTGCTG 288
 Oy 327 CCACGTGGTCTTCCAGCTCTGTGGCAGATGTGTACCCCGAGGGGTTCCAGGGCTGTGTC 386
 Db 289 CCGGTGGTCTTCCAGCTCTGTGGGATATATACCCCTGAGGGGTTATTGGACCTGTGTC 348
 Oy 387 CCTCACCCCGGGGACCTGAGAGAGAGAGAGTCCCTGTGCCAAGGAAATATTAACAC 446
 Db 349 CCTCACCTAGGGGACAGAGAGAGAGAGATGTGTGTGTCTCCCAAGGAAATATATTCAC 408
 Oy 447 CCGAATAATGACACATTGTGTGACCAAGTGCCCAAAAGGTACTTATCTGTACAAATGAC 506
 Db 409 CCTCAATAATATTGATTTGTGTACCAAGTGCCCAAAAGGAACTACTTGTACAAATGAC 468
 Oy 507 TGTCCGGTCCAGGGCCAGAGACAGACCTGACGGGTGTGTGCTCCCTGACCTTACCTGACC 566
 Db 469 TGTCCAGGCGCGGAGAGATACGACCTGACGGGAGTGTGAGCGGTCTCTTACCGCT 528
 Oy 567 TTGGAGAACATCTCAGACGATGCTGAGCTGTCCAGGTGCGGGGACGAATGTTCCAG 626
 Db 529 TCAGAAACACCTCAGACACTGCTCAGCTGTCCAAATGCCAAGGAAATGTTGTCAG 588
 Oy 627 GTGAGATTTCGCTGTGTAGTGTGACCGGACACTGTGTGCGGCTGACGAGAAACAG 686
 Db 589 GTGAGATCTTCTTGTGACAGTGACCGGGACACCGTGTGTGCTGACGAGAAACAG 648
 Oy 687 TACCGGAAATCTGGGGTGAATCTGCGTCCGGTGTCTGAATCTGACCTGTCTCCAAAT 746
 Db 649 TACCGGATTTATGTGAGTGAATACCTTTTCCAGTCTTCAATTCAGCTGTGCTCCAAAT 708
 Oy 747 GGCACAGGAAATATCCCTGCGCAGAGACAGACGACACATCTGACCTGACATATGAGGC 806
 Db 709 GGCACCGTGCACCTCTCTGCGCAGAGAAACGAAACACCGTGTGACCTGACATATGAGGT 768
 Oy 807 TTTCTTTCTTAAAGCGCGCAAGTGATCTCTGTGATGTGAATGTGAAGAA--CAAGAGTGC 863
 Db 769 TTTCTTTCTTAAAGAAAGAGAGTGTGTCTCTGTGTGAATGTGAAGAAAGCTGAGAGTC 828
 Oy 864 GAGAGTTATGTCCACCGGACCTTCAAGTGTGAAGCTCTGAGAGCCGAGGACATCA 923
 Db 829 ACGAAGTGTGTCTTACCCAGATTTGAGATTTAAGGACATGAGAGCTCAGGACACCA 888
 Oy 924 GTACTATTACCCCTGTGTGATTTGTCTGGGCTTTGCTGGACATCTTGCCTGTGCTGTC 983
 Db 889 GTGCTGTTGCCCTGTGTGATTTTCTTTGTGTGCTTTTATCCCTCTCTTATTTGTT 948
 Oy 984 TTACATGTGTCTTACCAAGGTTGAGAGCCCAAGCTTACTATCTATCTATTTGCGGAGTGC 1043
 Db 949 TTAAATGTATCTCTTACCAAGGTTGAGAGCTTACTATCTATTTTGTGAGAAATGTG 1008
 Oy 1044 ACTGTGTAAAGAGGGGAGCCAGAA-----CTCTGTGTGCGGCGCCAGGCTTC 1094
 Db 1009 ACACCTGAAAGAGGGGAGCTTGAAGAACTACTACTAAGCCCTTGGCCCCAAACCA 1068
 Oy 1095 AACCCACCAACACATCTGTGCTTACGCTTCAACCCCAAGTTTCAAGTCTGTCTTCAATCC 1154
 Db 1069 AGCTTCAGTCCCATCCAGGCTTCACCGCCACCTGGGCTTCAATCCGTCAGATTCC 1128
 Oy 1155 CCTTACATCTCTGTGACCGGTCCAACTTCCGAG-----CGGTGCAATCTCTCTCC 1205
 Db 1129 ACCTTCACTCTCACTCCACTATATACCCCGGTACTGTCTCCAACTTGTCCGCTCCGCG 1188
 Oy 1206 AGCAGAGCGGCGCGCCCATCTAAAGCTGTGAGCCCAATCTCCGCGGGGCTCCGCGCTCC 1265
 Db 1189 AGAAGGTGTGACCACTTATCAAGGGGCTGATACCCCATCT----- 1229
 Oy 1266 ACCCACTCTGTACCCCGGAGCTTCCGAGCTTCAACCAACTTGTATCCCGGAGGCTTCCG 1325
 Db 1230 -----TGGACAGGCTTC 1242
 Oy 1326 GCTTCCACCACTCTGTGACCCCAAGTTTCAAGAGTGGAGAGCCAGGCGCCCAAGGCGCC 1385
 Db 1243 GCTTCCGACCCCATCTCCCAACCCCTTCCAGAAAGTGGAGAGCAGCGCCCACA---AGCCA 1299


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QY 1386 GATCAGCTCGCGAATCCGACCCCGACCTCTTACGGCTGTGAGACGCGCTGCCCG 1445
Db 1300 CAGAGCCCTAGACACTGATGATACCCCGACGCTGTACGCGTGTGAGAACGTGCCCG 1359
QY 1446 TCGGCTGGAAGAGATTGTGCGGCGCTGGAGACTGACGACGACAGATGAGAGGCTG 1505
Db 1360 TTGCGCTGGAAGAGATTGTGCGGCGCTGGAGACTGACGACGACAGATGAGAGGCTG 1419
QY 1506 GAGCTGGAAGAACGAGCGCCCACTTGTGCGAGGCGAGTACAGCATGCTGGCGCTGCGG 1565
Db 1420 GAGCTGGAAGAACGAGCGCGCTTGTGCGAGGCGAGTACAGCATGCTGGCGACTGAGAG 1479
QY 1566 CGGCGGACGCGCGCGCGCGAGGCGACGCTGAGCTGTGGGCGCGCTCTCAAGAGCATG 1625
Db 1480 CGGCGGACGCGCGCGCGCGAGGCGACGCTGAGCTGTGGGCGCGCTCTCGCGACATG 1539
QY 1626 GACCTGCTGGGTTGCTGTGGAAGAACATGAGAGAGGCGTGGGCGCGCGCGCTCTCGG 1685
Db 1540 GACCTGCTGGGTTGCTGTGAGAGACATGAGAGAGGCGCTTTCGCGCGCGCGCTCTCGG 1599
QY 1686 TCCGAGCCCCCGCTTCTGTGTGAGAGCCCGCCCTCCGACTGGGCGCTCCCGCGCTG 1745
Db 1600 CCGCGCGCCCACTCTTCTGATGAGAGCGCGCCCTCGCGGCGAGCTCTAAGAGACGCTCTG 1659
QY 1746 C 1746
Db 1660 C 1660

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RESULT 15

AAQ10955 ID AAQ10955 standard; cDNA; 2111 BP.

XX AC AAQ10955;

DT 09-JAN-2003 (updated)

DT 24-MAY-1991 (first entry)

XX DE Encodes human 55kD TNF-binding protein.

KW Tumour Necrosis Factor; binding proteins; septic shock;

KW autoimmune glomerulonephritis; lymphokine; cytokine.

XX OS Homo sapiens.

FH Key Location/Qualifiers

FT sig_peptide /.*tag= a

FT mat_peptide /.*tag= b

FT /product= 55kD TNF-BP

XX PN EP417563-A.

XX PD 20-MAR-1991.

XX PF 31-AUG-1990; 90EP-0116707.

XX PR 20-APR-1990; 90CH-0001347.

XX PR 12-SEP-1989; 89CH-0003319.

XX PR 08-MAR-1990; 90CH-0000746.

XX PA (HOFF) HOFFMANN-LA ROCHE AG.

XX PI Brockhaus M, Dembic Z, Gentz R, Leselauer W, Lotscher H;

XX PI Schlaefer EU;

XX DR WP1; 1991-081851/12.

XX DR P-PSDB; AAR11082.

XX PT Insoluble tumour necrosis factor binding proteins - and DNA

XX PT encoding them, useful in pharmaceutical prods. and for antibody

```

PT prodn.
PS Claim 4; Fig 1; 26pp; German.
XX
CC Partial amino acid sequences were determined for the 55 and 75kD
CC TNF-BPs (see AAR1072-R11081) and oligonucleotide primers were
CC synthesized based on these partial sequences. The primers were used
CC to produce a cDNA fragment for use as a probe to screen a human
CC placental cDNA bank constructed in lambda g11. Positive clones were
CC identified and sequenced. DNA constructs comprising the TNF-BP coding
CC sequence may also contain a fragment encoding a human Ig domain.
CC Recombinant constructs are used to transform cells to confer
CC improved TNF-binding properties.
CC See also AAQ10956.
CC (Updated on 09-JAN-2003 to add missing OS field.)
SQ Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T; 0 other;
Query Match 29.7%; Score 724.2; DB 12; Length 2111;
Best Local Similarity 70.0%; Pred. No. 1,1e-138;
Matches 1119; Conservative 0; Mismatches 388; Indels 92; Gaps 7;

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QY 148 TGTCCCGCCCGCACTCAACCTCCACTCCCGACCCGAGGCGCGGCTCCACTGGCA 207
Db 41 TCTTATGCGCGAGTCTCAACCTCCACTCCCGACCCGAGGCACTTGGAGCTCTGAC 100
QY 208 TACGCGAGCACCGTGTGTCTGTCACTGTGCGGCGCGCACCTGCC-CAGCGCTGATGG 266
Db 101 AGACCGAGTCCCGGAGAGCCCGACACTGCGCGCTGCGCACCTGCCCTGAGCCCAATGG 160
QY 267 GATTTGAGAGGCCACAGCTGCGCGGACATGCGCTGCCACCGCTGCGCTGCTGCTG 326
Db 161 GAGTGTAGAGGCCACATGCTGCTGCG-CATGGCGCTTCCACCGCTGAGCTGCTGCTG 219
QY 327 CCACTGTGCTTCCAGCTCTGTGTGAGATGTGTATCCCGGAGGGTTCAAGGGCTGTC 386
Db 220 CCGTGTGTGCTCTGTGAGCTGTGTGTGGAATATATCCCTCAGGGGTTATTTGAC 279
QY 387 CCTCACCCCGGGGACCTGTGAGAGAGAGAGTCCCTGCTCCCAAGGAAATATATACAC 446
Db 280 CTTCACTAGGGGAGCAGGAGAGAGATGTGTGTGTCCCAAGGAAATATATACAC 339
QY 447 CCGGAAATATGACCATTTGCTGTGACCAAGTGCACAAAGATCTATCTGTACATGAC 506
Db 340 CTTCAATATATGATTTGCTGTGACCAAGTGCACAAAGATCTATCTGTACATGAC 399
QY 507 TGTTCGGGTCCAGGGCAGAGACGAGATGTGAGGCTGTGCTCCCTGCACTTACCTGCC 566
Db 400 TGTTCAGGGCCCGGGCAGAGATGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCT 459
QY 567 TTGAGAACCATCTCAGACGATGCTGAGCTGTGCGAGTGCAGGGGCGGAAATGTTCCAG 626
Db 460 TCGAANAACCATCTCAGACGATGCTGAGCTGTGCGAGTGCAGGAAATGAGGTGCG 519
QY 627 GTGAGATTTGCGCTTGTGTAGTGAACCGGAGACCTGTGTGCGCTGCAGAGAGAACAG 686
Db 520 GTGAGATTTGCGCTTGTGTAGTGAACCGGAGACCTGTGTGCGCTGCAGAGAGAACAG 579
QY 687 TACCGGAAATACGGGTGAAATCGCTTCCGCTGTGAACTGACGCTGTGCTCCAT 746
Db 580 TACCGGAAATACGGGTGAAATCGCTTCCGCTGTGAACTGACGCTGTGCTCCAT 639
QY 747 GGCACAGTGAATATCCCTGCGCAGAGAGACAGGACCAATGCGCACTGCCATATGGGC 806
Db 640 GGCACAGTGAATATCCCTGCGCAGAGAGACAGGACCAATGCGCACTGCCATATGGGC 699
QY 807 TTTCTTTTAAAGCGCCAGATGCTCTGTGATGATTTGAGAA---CAAGAGTGC 863
Db 700 TTTCTTTTAAAGAGAAAGAGTGTGCTCTGTGATGATTTGAGAAAGCTGTGAGTGC 759
QY 864 GAGAGATTATGTCCACCGACCTTCACTGTGTAAGACTCTCAGAGCCAGGACTTACA 923
Db 760 ACGAGTTGTGCTTACCCAGATTGAGAAATTTAAGGGCAGTGAAGGACTGAGGACGACACA 819

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OY 924 GTACATTAACCCCTGGTGAATTTGCTTCGGGCTTGGCTGGATCCTTGCCCTGTCTGTC 983
DB 820 GTGCTGTGCCCCCTGGTCAATTTCTTTGGTGTGGCTTTTATCCCTCTTCAATGGT 879
OY 984 TTAGCATGTGGTACACGCGGTGAGGCCAAGCTCTACTCCATCATTTTGGCGAGTCG 1043
DB 880 TTAATGTATCGGTACCAAGGTGAAAGTCCAAAGCTCTACTCCATGTGTTGGGAAATCG 939
OY 1044 ACTCTGTAAAAGAGGGGAGCCAGAA-----CTCTGTGTCCGGCCCAAGCTTC 1094
DB 940 ACACCTGAAAAAGAGGGGAGCTTGAAAGAACTACTAAGCCCTGGCCCAAAACCA 999
OY 1095 AACCCACCAACACCATCTGCTTCAAGCTCAACCCCAAGTTCAGTCTGTCTCCATTC 1154
DB 1000 AGCTTCACTCCATCTCAAGGCTTCAACCCCACTGGGCTTGAGTCCGATGCCAGTTC 1059
OY 1155 CTTACATCTCTGTGACCGGTCCAATCTTGGAG-----CCGTGCAATCTCCCTCC 1205
DB 1060 ACCTTCACTCCAGCTCAACCTATACCCCGGTGACTGTCCAACTTTGGCGCTCCCGC 1119
OY 1206 AGCGAGAGGCCCCCGCCCATTTAAAGGTGGCCCATCTTCGCGGAGCTTCGCGCTCC 1265
DB 1120 AGAGAGGTGGCAACCCCTATCAGGGGGCTGACCCCATCTTGCAGACAGCCCTCGCTCC 1179
OY 1266 ACCCACTCTGATCCCGGGGCTCGGGCTCCACCACTCTGTATACCCCGGGGCTCCG 1325
DB 1180 GACC----- 1183
OY 1326 GCCTTCACCACTCTGCAACCCCAAGTTCAGAAAGTGGAAAGCCAGCCGCCGCCCC 1385
DB 1184 -----CGATCCCAACCCCTTCAAGATGGAGAAAGAGCCCAACA--AGCCA 1230
OY 1386 GATCAGCTCGCGAATGCCGACCCCGGACCTGTACGCGGTGTGGAACGCGCTGCCCG 1445
DB 1231 CAGAGCCTTAGACACTGATGACCCCGGACGCTGTACGCGGTGTGAGAAACGTGCCCG 1290
OY 1446 TCGGCTGGAAGAGTGGTGGCGGCGCTGGGACTGAGCGAGACAGATGAGCGGCTG 1505
DB 1291 TTGCGCTGGAAGAAATTCGTGGGCGCTTAGGGCTGAGCGACACGAAATCGATGGCTG 1350
OY 1506 GAGCTGAGAAACGGCGGCGCACCTGCGCGAGGCGCAGTAACGATGCTGGCGCTGGCGG 1565
DB 1351 GAGCTGAGAAACGGCGGCGCTGGCGGAGGCGCAATACGATGCTGGCGACTGGAGG 1410
OY 1566 CGGCGCAACGCGCGCGCGAGGCGCAGCTGAGCTGTGGGCGCGCTGCTCAGGSAATG 1625
DB 1411 CGGCGCAACGCGCGCGCGAGGCGCAGCTGAGCTGTGGGAGCGCTCTCGCGACATG 1470
OY 1626 GACCTGTGGGTTGGCTGGAATAATAGAGAGGCGCTGGGTGGCGCGCCGCGCTGGCG 1685
DB 1471 GACCTGTGGGTTGGCTGGAAGCAATCAAGAGGCGCTTTGGGCGCGCCGCGCTCCCG 1530
OY 1686 TCCGAGCCCGGCTTCTGTGTGAAGCCCGCCCTCCG 1724
DB 1531 CCGGCGCCCAAGTCTTCAGATGAGGCTGGCGCCCTGGCG 1569
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Search completed: September 15, 2003, 05:11:31
Job time : 483 secs

QY 301 TCCCAACGAGGCTGAGCTGCTGCTGCACTGCTGCTTCCAGCTCTGTTGGCAGATGTGT 360
DB 301 TCCCAACGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 ACCCGCAGAGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 ACCCGCAGAGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 CCTGTCCCAAGGAAATATTAACACCCGCAAAATAGCAACATTTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 CCTGTCCCAAGGAAATATTAACACCCGCAAAATAGCAACATTTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 ACAAAAGTACTATCTGTAACATGACTGTCCGGGTCCAGAGGCAAGCAAGCAAGCAAGCAAGCA 540
DB 481 ACAAAAGTACTATCTGTAACATGACTGTCCGGGTCCAGAGGCAAGCAAGCAAGCAAGCAAGCA 540
QY 541 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 CCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 CTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 CTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GTCTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 GTCTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 ACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 ACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 ATGATTTGAAGAACAGAGAGTGCAGAGATTAATGTCACACCCGCACTTCACTGCTGCTGCTGCT 900
DB 841 ATGATTTGAAGAACAGAGAGTGCAGAGATTAATGTCACACCCGCACTTCACTGCTGCTGCTGCT 900
QY 901 ACTCTGAGAGCCGAGGCACTACAGTACTAATACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 ACTCTGAGAGCCGAGGCACTACAGTACTAATACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 TGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
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DB 1141 CTGTCTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 CCTCAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
DB 1201 CCTCAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
QY 1261 CCTCAGAG 1320
DB 1261 CCTCAGAG 1320
QY 1321 CTGCGGCTGCAACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 CTGCGGCTGCAACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

QY 1381 CCCCCGATCAGCTGCGGAGTGCAGACCCCGGAGCCTCTGAGCGGTGTGAGCGGCTGCTG 1440
DB 1381 CCCCCGATCAGCTGCGGAGTGCAGACCCCGGAGCCTCTGAGCGGTGTGAGCGGCTGCTG 1440
QY 1441 CCCCCGATCAGCTGCGGAGTGCAGACCCCGGAGCCTCTGAGCGGTGTGAGCGGCTGCTG 1500
DB 1441 CCCCCGATCAGCTGCGGAGTGCAGACCCCGGAGCCTCTGAGCGGTGTGAGCGGCTGCTG 1500
QY 1501 GACTGAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
DB 1501 GACTGAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
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DB 1561 GAG 1620
QY 1621 ACATGAGCT 1680
DB 1621 ACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 TGGGCT 1740
DB 1681 TGGGCT 1740
QY 1741 CCTGCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
DB 1741 CCTGCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 TGTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
DB 1801 TGTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 1861 GATCTGCGAGGCT 1920
DB 1861 GATCTGCGAGGCT 1920
QY 1921 TGAATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
DB 1921 TGAATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
QY 1981 TGTGCT 2040
DB 1981 TGTGCT 2040
QY 2041 CCAAGGAGGCT 2100
DB 2041 CCAAGGAGGCT 2100
QY 2101 GAGAACTCAGAGG 2160
DB 2101 GAGAACTCAGAGG 2160
QY 2161 ATAAAGCATCTTTGATCACTCTGCACTGCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 2220
DB 2161 ATAAAGCATCTTTGATCACTCTGCACTGCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 2220
QY 2221 CTTTGTGCT 2280
DB 2221 CTTTGTGCT 2280
QY 2281 TGGGAGCT 2340
DB 2281 TGGGAGCT 2340
QY 2341 CTTTGTGCT 2400
DB 2341 CTTTGTGCT 2400
QY 2401 CTGCGGCTGCAACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
DB 2401 CTGCGGCTGCAACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460

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RESULT 2
US-08-321-668-1
: Sequence 1, Application US/08321668
: Patent No. 5665859
: GENERAL INFORMATION:
: APPLICANT: WALLACH, David
: APPLICANT: BRAKEBUSH, Cord
: APPLICANT: VARFOLOMEY, Eugene
: APPLICANT: BAIKIN, Michael
: TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
: TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/321,668
: FILING DATE: 12-OCT-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 107268
: FILING DATE: 12-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: WALLACH-13
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2175 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 256..1620
: US-08-321-668-1

Query Match          29.8%; Score 727; DB 1; Length 2175;
-Best Local Similarity 69.6%; Pred. No. 5,4e-150; Indels 92; Gaps 7
Matches 1129; Conservative 0; Mismatches 400;

Qy 148 TGTCCGCCCCCGACGTCGACACCTCCACCTCCCGACCGGAGCCCGGCGCTCCACTGGGCA 207
Db 110 TCTCTATGCCGAGGTCGACACCTCCACCTGTCACCCCAAGACCTTGGACGCTCTCGAGC 169
Qy 208 TACGCGAGGACCGTGTGTGCTGTCACCTGTCGCGGGCGCCGACCTGCC-CAGCCCTGATGGG 266
Db 170 AGACCGAGTCCCGGGAGACCCCGACGACCTGCGCGCTGCACACATGCCCTGAGCCCAATGGG 229
Qy 267 GGATTGAGAGGCGACAGCTGCGCGGCGGACATGGGCGCTCCGACCGTGCCTGCTGCTGTC 326
Db 230 GGAAGTGAAGGCGCATAGCTGTGTGG-CATGGGCTCTCCACCGTGCCTGACCTGCTGCTG 288
Qy 327 CCACTGTGCTTCCAGCTCTGTTGGCAGATGTGTAACCCCGCAGGGGTTTCAAGGGGCTGTGC 386
Db 289 CCGCTGTGCTCTCTGAGACTGTGTGGGAAATATACCCCTCAGGGGGTTATTGACTGTGTC 348
Qy 387 CCTCAGCCCGGGGACCTGAGAGAGAGAGAGAGTCCCTGTCCCAAGAAATATTAACAC 446

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QY 1155 CCTTACATCTCTGTGACCGGCTCCAACTTCGAG-----CGGTGCATCTCCCTCC 1205
 Db 1129 ACCCTTACCTTCAGAGCTCACCTATATACCCGGGTACTGTCCTCACTTTGGGGCTCCCGC 1188
 QY 1206 AGCGAGACGGCCCGCCCATCTTAAAGCTGGCCCATCTCTCCGGGGCCCTCCGGCTCC 1285
 Db 1189 AGAGAGGTGGACACCTCTATCAGGGGGCTGACCCCTCTCT-----1229
 QY 1266 ACCCACTCTGTACCCCGGGGGCTCCGGGCTCCACCACTCTGTACCCCGGGGCTCCG 1325
 Db 1230 -----TGGACAGCCCTC 1242
 QY 1326 GCTTCCACCACTCTGTACACCCAGTTTCAAGTGGAGACGAGCCCGCCCGCC 1385
 Db 1243 GCTTCCACCACTCTGTACACCCAGTTTCAAGTGGAGACGAGCCCGCCCGCC---AGCCA 1299
 QY 1386 GATCAGCTCCGGATGCGGACCCCGGACCTCTGACCGGCTGTGTGACAGCGCTGCCCCG 1445
 Db 1300 CAGAGCTTACAGACTGATGACCCCGGACGCTGTACCGCTGTGTGAGAAAGTCCCGC 1359
 QY 1446 TCGGCTGAGAGAGTGTGCGGCGCTGGGACTGAGCGAGACGAGATGAGCGGCTG 1505
 Db 1360 TTGCGCTGAGAGAGTGTGCGGCGCTGGGACTGAGCGAGACGAGATGAGCGGCTG 1419
 QY 1506 GAGCTGAGAGACGGGCGGCACTGCGGAGCGGAGTACAGACTGTGCGGCGCTGCGG 1565
 Db 1420 GAGCTGAGAGACGGGCGGCTGCTGCGGAGCGGAGTACAGACTGTGCGGCGCTGCGG 1479
 QY 1566 CGGCGACCGCGCGCGCGGAGGCGACGCTGAGAGTGTGCGGCGCGCTGCGGAGT 1625
 Db 1480 CGGCGACCGCGCGCGCGGAGGCGACGCTGAGAGTGTGCGGCGCGCTGCGGAGT 1539
 QY 1626 GACCTGTGGGTTGCTGGAAGAAATAGAGAGGCGCTGGTGGCGCGCGCGCTGCGG 1685
 Db 1540 GACCTGTGGGTTGCTGGAAGAAATAGAGAGGCGCTGGTGGCGCGCGCGCTGCGG 1599
 QY 1686 TCCGAGCCCGGCTTCTGTGTGAGGCGCGCGCTGCGAGCTGCGGCGCTGCGGCGCTG 1745
 Db 1600 CCGCGCGCGGCTTCTGTGTGAGGCGCGCGCTGCGAGCTGCGGCGCTGCGGCGCTG 1659
 QY 1746 C 1746
 Db 1660 C 1660

RESULT 4
 US-08-126-016-1
 : Sequence 1, Application US/08126016
 : Patent No. 5811261
 : GENERAL INFORMATION:
 : APPLICANT: WALLACH, DAVID
 : APPLICANT: NOPAR, YARON
 : APPLICANT: KEMPER, OLIVER
 : APPLICANT: ENGELMANN, HARTMUT
 : APPLICANT: BRAKEBUSCH, CORD
 : APPLICANT: ADERKA, DAN
 : TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
 : NUMBER OF SEQUENCES: 26
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Browdy and Neimark
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/126, 016
 FILING DATE: 24-SEP-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/625668
 FILING DATE: 13-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, ROGER L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: WALLACH4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248631
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2175 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 256..1620
 NAME/KEY: mat_peptide
 LOCATION: 319..1620
 US-08-126-016-1

Query Match 29.8%; Score 727; DB 1; Length 2175;
 Best Local Similarity 69.6%; Pred. No. 5,4e-150;
 Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

QY 148 TGTCCCGCGCCGAGTCTCAACCTCCACCTCCGACCCGAGGCGCGGAGCTCACTGAGCA 207
 Db 110 TCTTTATGCCGATCTCAACCTCAACCTCAACCTCAACCTCAACCTCAACCTCAACCT 169
 QY 208 TACCGGAGACCGTGTGTCTGCTCACTGTGCGGCGCGGCGGCGGCGGCGGCGGCGG 266
 Db 170 AGACCGAGTCCCGGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 229
 QY 267 GATTTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 326
 Db 230 GAGGTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 288
 QY 327 CCACTGTGCTCCAGCTCTGTGTGCGGAGTGTATCCCGGAGGAGGTTTCAAGGCGGCTG 386
 Db 289 CCGTGTGCTCTCTGAGCTGTGTGTGAGATATACCTCTCAAGGAGGTTTATGAGCTGTC 348
 QY 387 CTTCAACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 446
 Db 349 CTTCACTAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
 QY 447 CCGCAAAATAGACCAATTTGCTGCGCAAGTGTCCCAAGGAGTCTTCTGTACATGAC 506
 Db 409 CTTCAAAATATATGATTTGCTGTACCAAGTGTCCCAAGGAGTCTTCTGTACATGAC 468
 QY 507 TGTCCGGGTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 566
 Db 469 TGTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 528
 QY 567 TTGAGAGACATCTCAGACGATGCTGCTGCTCAAGTGTCCGCGGCGGCGGCGGCGGCGG 626
 Db 529 TCAAGAAACCACTCAACACTGCTCAAGTGTCCGCGGCGGCGGCGGCGGCGGCGGCGG 588
 QY 627 GTGAGATTTGCTGCTGT 686
 Db 589 GTGAGATTTGCTGCTGT 648
 QY 687 TACCGGAGATCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 746
 Db 649 TACCGGAGATTTGAGATGAAACCTTTTCCAGTGTCTTCAATTCAGGCTCTGCTCAAT 708


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747 GGCACAGTGAATATCCCTGCGAGAGAGACAGACACCATCTGCCATCTCATATGAGC 806
709 GGGACCGGTGACCTCTCCCTGCGAGAGAAACAGAACACCGTGTGACCTGCATGACGT 768
807 TTCTTTTCTTAAGGGCCCAAGTGCATCTCTGTCAATGATTTGAAGAA---CAAGAGTGC 863
769 TTCTTTCTTAAGGAAACAGAGTGTCTCTCTAGTAACTGTAAGAAAGCCTGAGTGC 828
864 GAGAATATATGTCGAACCGACCTTCACTGTGTAAGACTCAAGACCCAGCACTCA 923
829 AGCAAGTTGTGCTTACCCCAATTAGAAATGTAAGGGAGTCAAGAGACTCAAGCA 888
924 GTACTATTAACCCCTGTGTATGTCTTCTGCGGCTTTCCTGCACTCCCTGTCTGTC 983
889 GTGCTGTGGCCCTGTGATTTCTTTGGTCTTTCCTTTATCCCTCTCTCAATGGT 948
984 TTAGCATGCTGTACCAAGGCTGGAAGCCCAAGCTTCACTCATATTTGGGGGCAATG 1043
949 TTAATGTATCGTTACCAAGGCTGGAAGCTCAAGCTTCACTCATATTTGGGGAAATG 1008
1044 ACTGTGTAAAGAGGGGGAGCCAGAA-----CTGCTGTGCGGGCCCAAGCTTC 1094
1009 ACACCTGAAAGAGGGAGGTTGAAGAACTACTAAGCCCTGAGCCCAAAACCA 1068
1095 AACCCCAACCAACCATCTGCTTCAAGTCAACCCCAAGTTCAGTCTGTCTCAATCCC 1154
1069 AGCTTCAGTCCCACTCAAGGCTTCAACCCCAACCTGGGCTTCAAGTCCGATGCC 1128
1155 CCTTACATCTCTGTGACCGGTTCACCTTGGAG-----CGTGTGATCTCTCTCC 1205
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1206 AGCGAGAGCGGCGCGCCCATCTAAAGGTGAGCCCATCTCCGCGGGCCCTCCGCTCC 1265
1189 AGAGAGGTGGACCAACCTATCAGGGGCTTACCCCACTCT-----1229
1266 ACCCACTCTGTACCCGCGGGCTTCGAGCTTCCACCACTCTGTATCCCGGGGCTTCG 1325
1230 -----TGGCAAGCCCTC 1242
1326 GCTTCCACCACTCTGTGACCCCACTTCAAGATGGAAGCCAGCGCCCAAGCGCCCC 1385
1243 GCTTCCGACCCCATCCTCAACCCCTTGAAGATGGAAGCAAGCGCCCAACA---AGCCA 1299
1386 GATCAGCTCGCGGATGCGGACCCCGGACCTGTACGCGGTGTGGAAGCGGCTGCCCG 1445
1300 CAGAGCCTAGACACTGATGACCCCGGACGCTGTACGCGGTGTGGAAGAGTGCCTCCG 1359
1446 TCGCGCTGGAAGAGTGTGTGCGGCGCTGTGGAAGTGAAGCAAGAGATCGAGCGCTG 1505
1360 TTGCGCTGGAAGAAATTTGTGCGGCGCTTGAAGGCTGAGCAACAGATCGATCGCTG 1419
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1420 GAGCTGGAAGAGCGGCGGCTGCGGCGGAGCGGCTGACAGATGCTGTGCGGCTGTGCGG 1479
1566 CGGCGCAAGCGGCGGCGGAGCGGAGCGGCTGTGAGGCTGTGCGGCGGCTGTGAGGAGATG 1625
1480 CGGCGCAAGCGGCGGCGGAGCGGAGCGGCTGTGAGGCTGTGCGGCGGCTGTGAGGAGATG 1539
1540 GACCTGTGCGGCTGTGAGGAGATGAGGAGGCGCTTTTGCGGCGGCGGCGCTTCGCG 1599
1686 TCGGAGCGGCGGCTGTGAGGAGATGAGGAGGCGCTGTGAGGCTGTGAGGAGATG 1745
1600 CCGCGCGGCGGCTGTGAGGAGATGAGGAGGCGCTGTGAGGAGATGAGGAGATG 1659
1746 C 1746
1660 C 1660

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RESULT 5
US-08-054-970-1
; Sequence 1, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: BROMDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,970
; FILING DATE: 03-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1620
; US-08-054-970-1

Query Match 29.8%; Score 727; DB 4; Length 2175;
Best Local Similarity 69.6%; Pred. No. 5,4e-150;
Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

148 TGTCCCGCCCGAGTCTCAACCTCCCACTCCCGAGCCGAGGCGCGGCTGCACTGGGCA 207
110 TCTCTATGCGCGAGTCTCAACCTCAACTGTACACCCCAAGCACTTGGAGCTCTGAC 169
208 TACGCGAGAACCGTGTGTGTCACTGTGCGGCGGCGCACTGCCC-CAGCCCTGATGG 266
170 AGACCGAGTCCCGGGAAGCCCAAGCACTGCGGCTGCGCACACTGCTGAGCCCAATGG 229
267 GATTTGAGAGGCCACAGCTGCGGAGATGGGCTTCCCAACCTGTGCTGTGCTGTG 326
230 GAGGTGAGAGCCATATACCTGTCTGG-CATGGGCTTTCACACCGGCTGTGACTGTGCTG 288
327 CCACTGTGCTTCCAGCTGTGTGGCAGATGTGTACCCCGAGGGGTTGAGGGGCTGTGCT 386
289 CCGGTGTGCTCTCTGAGCTGTGTGTGGAAATATACCCCTCAAGGGATTATGACTGTG 348
387 CTTCAACCCCGGAGACTGTGAGAAAGAGAGAGTCCCTGTGCCAAGGAAATATACAC 446
349 CTTCACTAGGAGGAGAGAGAGAGATATGTGTGTCCCAAGGAAATATATCAC 408
447 CCGGAAATATAGACATTTGTGTGACCAAGTGTGCAAAAGTACTTATCTGTACATGAC 506
409 CTTCAAAATATTTGATTTGTGTGTACCAAGTGTGCAAAAGAACTTATCTGTACATGAC 468

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QY 507 TGTCCGGGTCAGGGGAGACAGGAGCTGAGGGTGTGCCCCCTGGCACTTACCTGCC 566
 DB 469 TGTCCAGGGCCCGGGGAGATACGGACTGCGAGGGAGGTGAGAGCGGCTCTTCAACCGCT 528
 QY 567 TTGGAGAACATCTGACGATGCGTGAAGTGTCTCCAGGTCGCGGAGACGAAATGTTCCAG 626
 DB 529 TCGAAAAACCACTCAGACACTGCTCAGCTGCTCCAAATGCCGAAAGAAATGGGTAG 588
 QY 627 GTGAGATTTTGGCTTTGTAGTGAACCGGAGACACTGTGCGGCTGACAGAAACGAG 686
 DB 589 GTGAGATCTCTTCTTGTGACAGTGGACCGGAGACCGGTGTGTGCTGACAGAAACGAG 648
 QY 687 TACCGGAAATAGTGGGGTGAATGCGCTTCGAGTGTCTGAACTGACGCTTGTCCAAAT 746
 DB 649 TACCGGCAATTATGAGATGAAACCTTTTCCAGTGTCTTCAATGACGCTTGTCCAAAT 708
 QY 747 GGCACAGTGAATATCCCTGCGGAGAGACAGAGACCAATTCGCCACTGCGCAATATGGC 806
 DB 709 GGGACCGTGAACCTCTCTTCCAGAGAGAAACAGAAACCGGTGACCTGCGCATGCAAGT 768
 QY 807 TTCTTTCTTAAAGCGCCCAAGTGCATCTCTGTGATGTATGAA---CAAGAGTGC 863
 DB 769 TTCTTTCTTAAAGAAAAAGAGTGTCTCTGTATGATGTATGAAAGGCTGGAGTGC 828
 QY 864 GAGAGATTATGTCCACCCGACCTTCACTGTAAGAATCTTCAGAACCCAGCACTACA 923
 DB 829 ACAGAGTTGTGCTTACCCAGATGAGAAATGTAAAGGCACTGAGGACTGAGCAGACACA 888
 QY 924 GTACTATTACCCCTGATGTTGTTGCGGCTTGTGCGATGCTTCCCTCTGTGTGTC 983
 DB 889 GTGTGTGCCCCGTGATTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 948
 QY 984 TTAGCATGTGCTTACAGCGGTGAGAGCCCAAGCTTACTTCACTTATTTGGCGGAGTGC 1043
 DB 949 TTATATATGTGCTTACAGCGGTGAGAGCTTACTTCACTTATTTGTGCGGAGTGC 1008
 QY 1044 ACTCTGTAAAGAGGGGAGAGCCAGAA-----CTCTGTGCTCCGCGCCCAAGGCTTC 1094
 DB 1009 ACACCTGAAAAAGGGGGAGGCTTGAAGAACTACTTAAAGCCCTGCGCCCAACCCA 1068
 QY 1095 AACCCGACCAACCACTTGTGTTGAGCTTCAACCCCAAGTTCGATGCTTGTCCATTC 1154
 DB 1069 AGCTTCACTGCTTCAAGGCTTCAACCCCAAGTTCGATGCTTGTCCATTC 1128
 QY 1155 CCTTACATCTCTTGAACCGGTTCACCTTGGAG-----CGGTGCTCTCTCCCTGC 1205
 DB 1129 ACCTTCACTGCTTCAAGGCTTCAACCCCAAGTTCGATGCTTGTCCATTC 1188
 QY 1206 AGCAGAGCGGCGCGCCCATCTTAAAGGCTGAGCCCATCTTCCGCGGCTTC 1265
 DB 1189 AGAGAGGTGGACCAACCTTATCAGGGGGCTGACCCCATCTT----- 1229
 QY 1266 ACCCACTCTGTACCCCGGGGCTTCCGCGCTTCAACCCCATCTTGTACCCCGGGGCTTCCG 1325
 DB 1230 -----TGTCAAGGCTTC 1242
 QY 1326 GCGTCCACCCCACTCTGCAACCCCAAGTTCAGAAAGTGGAGAGCGGCGCCGAGCGCC 1385
 DB 1243 GCGTCCACCCCACTCTGCAACCCCAAGTTCAGAAAGTGGAGAGCGGCGCCGAGCGCC 1299
 QY 1386 GATCAGCTCGGAGATGCGGACCCCGGACCTTGTACCGGAGTGTGAGAGCGGTGCCCCG 1445
 DB 1300 CAGAGCTTACGATGATGAGCCCGGACGCTGTACCGGAGTGTGAGAGAGTGTCCCCG 1359
 QY 1446 TCGGCTGAGAGAGTGTGAGGCGGCTGAGGACGAGGAGAGAGAGAGAGAGAGAGAGAG 1505
 DB 1360 TTGCGCTGAGAGAGTGTGAGGCGGCTTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1419
 QY 1506 GAGCTGAG 1565
 DB 1420 GAGCTGAG 1479
 QY 1566 CCGGCGCAGCGCGCGCGCGGAGGCGACGCTGAGAGCTGTGCGCGCGGCTGTACGAGGAGATG 1625

DB 1480 CCGGCGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1539
 QY 1626 GACCTGTGGGTTGCTTGTGAAACATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1685
 DB 1540 GACCTGTGGGTTGCTTGTGAAACATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1599
 QY 1686 TCGAGCGCGCGGCTTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1745
 DB 1600 CCGGCGCGGCGGCTTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1659
 QY 1746 C 1746
 DB 1660 C 1660
 RESULT 6
 US-09-106-038A-1
 ; Sequence 1, Application US/09106038A
 ; Patent No. 6007995
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenda F. Baker and Lex M. Cowser
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
 ; NUMBER OF SEQUENCES: 91
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Isis Pharmaceuticals, Inc.
 ; STREET: 2292 Faraday Avenue
 ; CITY: Carlsbad
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92008
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows NT
 ; SOFTWARE: Microsoft Word, 97
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/106,038A
 ; FILING DATE: June 26, 1998
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Laurel Spear Bernstein
 ; REGISTRATION NUMBER: 37,280
 ; REFERENCE/DOCKET NUMBER: RTS-0004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (760) 931-9200
 ; TELEFAX: (760) 603-3820
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2161
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-106-038A-1
 Query Match 29.7%; Score 725.8; DB 3; Length 2161;
 Best Local Similarity 70.0%; Pred. No. 9,9e-150;
 Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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DB 289 CCGGCTGGTCTCTGGAGCTGTGTGGAAATATACCCCTGAGGGTTATTGACTGTGTC 348
OY 387 CCTACCCCGGGGACCTGGAGAGAGAGAGTCCCTGTCCCAAGAAATATATACAC 446
DB 349 CCTCACCTAGGGGACAGGAGAGAGAGATAGTGTGTCTCCCAAGAAATATATATCAC 408
OY 447 CCGCAAAATAGACCATTTGTCTGACCAAGTGCACAAAGGATCTATCTGTACAAATAC 506
DB 409 CCTCAAAATATTCATTTTGTCTGTACCAAGTGCACAAAGGATCTATCTGTACATAC 468
OY 507 TGTCCGGGTCCAGGGCAGAGACAGGACTGCAAGGTGTGTGCCCCCTGGACCTTACATCC 566
DB 469 TGTCCAGGCCCGGGCAGAGATACGACTGCAAGGAGTGTGAGAGGGCTCTTCAACGCT 528
OY 567 TTGAGAAACCATCTACAGAGATGTCTGAGCTGTCTCAGGTCCGGGACGAAATGTTCCAG 626
DB 529 TCAGAAACCACTCAGACACTGCTCAGCTCTCAATATGCCAAAGAAATGGGTGAG 588
OY 627 GTGAGATTTTGCCTGTGTAGTGGACGGGGAACATGTGTGCGGTGAGAGAAAGAACAG 686
DB 589 GTGAGATCTCTTCTTTCAGACAGTGGACGGGACACCGGTGTGTGCTGAGAGAAACAG 648
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DB 769 TTCTTTCTTAAAGAAAGAGAGTGTCTCTCTGTATGATCTGTAAAGAAAGCTGTAGTGC 828
OY 864 GAGAAATATGTCCAAACCCGACCTTCAACTGTGTAAAGACTCTCAGAGCCAGGCACTACA 923
DB 829 ACGAAGTGTGCTCTACCCCAATGAGATGTAAGGACACTGAGGACTCAGGACCCACA 888
OY 924 GTACATATACCCCTGTGTATGTTGTCTTGGGGCTTGGCTGCACTCTTGGCTGTGTGCTC 983
DB 889 GTGCTGTGCCCCCTGTGTATTTTGTGTCTTGTGCTTTTATCTCTCTCTCTTCAATGAT 948
OY 984 TTAGCATGTGCTACACAGCGGTGAGAGCCAAAGCTCTACATCATTTGGGGGCACTGCG 1043
DB 949 TTAATGTATGCTACCAAGGTGTGAGAGTCAAGCTCTACATCTCATTTGTTGTGGAAATCG 1008
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DB 1009 ACACCTGAAAAAGGGGGGAGCTTGAAGAACTACTACTAAGCCCTGGCCCCCAACCA 1068
OY 1095 AACCCCAACCAACCATCTGCTTTCAGCTTCAACCCCAATTCAGTCCGTCTCAATTCGC 1154
DB 1069 AGCTTCAATGCTCCACAGGCTTCAACCCCAACCTCGAGCTTCAAGTCCGTGCCCAAGTTC 1128
OY 1155 CCTTACATCTCTGTGACCGGTCTCAATTCGAG-----CGGTGCACTTCTCCCTCC 1205
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DB 1230 -----TGCACACGCTTC 1242
OY 1326 GCTTCACACCACTCTGACACCCCAATTCAGAGTGGAGAGCCAGGCCCAAGGCCCC 1385
DB 1243 GCTTCACACCACTCTGACACCCCAATTCAGAGTGGAGAGCCAGGCCCAAG-----AGCA 1299
OY 1386 GATACGTCTGGGATGCGAGCCCGGCACTCTGTACGGGGTGTGAGAGGGGCTGCCCCG 1445
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DB 1300 CAGAGCTTACACTGATGACCCCGGACGCTGTACGCCCTGTGTGAGAAAGTGTCCCCG 1359
OY 1446 TCGGCTGGAAGAGATTGTGTGTCGGCGGCTGTGAGCTGAGCGAGACAGATGAGCGCTG 1505
DB 1360 TTGCGCTGGAAGAAATTCGTGCGGCGCTGAGGGCTGTAGCGACACAGATGATCGGCTG 1419
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DB 1600 CCGCGCCCAAGTCTTCTGATGAGGCTGTGCGCTGTGCG 1638

RESULT 7
US-09-505-250-3
; Sequence 3, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: . FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2161
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(1623)
US-09-505-250-3

Query Match 29.74; Score 725.8; DB 4; Length 2161;
Best Local Similarity 70.04; Pred. No. 9.9e-150;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

DB 148 TGTCCCGCCCGAGTTCACACCTCCCACTCCCGACCCGAGGCCCGGAGCTTCACTGGCA 207
DB 110 TCTTATGCCCCGAGATCTCAACCTCAACTGTACACCCCAAGCACTTGGAGCTGTGAC 169
OY 208 TACGCGAGAACCGGTGTGTCTGCTGCTGCTGCGGGGCGGCACTGTGCC-CAGCCCTGATGG 266
DB 170 AGACCTAGTCCCGGAGAGGCCCAAGCACTGTGCGCTGCACTGTGCCCAAGTGG 229
OY 267 GATTTGAGAGGCCACAGCTGTGCGGACATGTGCTTCCCACTGTGCTGTGCTGTGCTG 326
DB 230 GAGGTGAGAGGCCCATAGCTGTGTG-CATGGGCTTCCACCGGCTGTGACTGTGCTG 288
OY 327 CCACTGTGTCTCAGCTGTGTGTGAGAGTGTGTACCCCGAGGGGTTTCAAGGGCTGTG 386
DB 289 CCGTGTGTGTCTTGTGAGCTGTGTGTGTGGAATATACCCCTCAGGGGTTATTGAGCTGTC 348
OY 387 CTTACACCCCGGAGCTGTGAGAGAGAGATCTCTGTCCCAAGAAATATATACAC 446
DB 349 CTTCACTAGGGGACAGGAGAGAGAGATAGTGTGTCTCCCAAGAAATATATATCAC 408
OY 447 CCGCAAAATAGACCATTTGTCTGACCAAGTGCACAAAGGATCTATCTGTACAAATAC 506
DB 409 CCTCAAAATATTCATTTTGTCTGTACCAAGTGCACAAAGGATCTATCTGTACATAC 468
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Qy	507	TTGTCGCGATCCAGGGGAGACAGGACTGAGAGGTGTGTGTCCTCCGACCTTCACTGACC	566
Db	469	TGTCTCAAGACCAGGGAGAGATACGAGACTGACGGAGATGTAGAGCCGCTCTTTCACCGCT	528
Qy	567	TTTGAGAACCATCTCAGACGATGCTGAGCTGTCTCCAGTGTCGGGAGCGAATGTTCAG	626
Db	529	TCAGAAAAACCACTCAGACACTGCTCAGCTGCTCCAAATGCGGAAAGAAATGGGTGAG	588
Qy	627	GTTGAGATTTTGGCTTGTGTGTATGTGACACCGGAGACCTGTGTGCGGCTTCAGAAAGAACAG	686
Db	589	GTTGAGATCTCTTCTTTCACAGTGTGACCGGAGACCGTGTGTGCTGTGACAGAAAGAACAG	648
Qy	687	TACCGGGAATACTGGGGTGAATACGGCTTCCGGGTGTCTGAATCTSCAGCTCTGTGCCAAT	746
Db	649	TACCGGCAATTATGTGATGTGAAAACCTTTCCAGTGTCTTCAATGTSCAGCTCTGCTCAAT	708
Qy	747	GGCACAAGTAAATATCCCTGTCCAGAGAGACAGGACCACTGTCCACTGTCCATATGGC	806
Db	709	GGGACCGTGAACCTCTCTCTGCCAGAGAAAACAGAAACCGGTGTGCACTGTCCATGACAGT	768
Qy	807	TTCTTTCTTAAAGGCGCAAGTGCATCTCTGTATGTGTATGAA---CAAGAGTGC	863
Db	769	TTCTTTCTTAAAGAAAAGAGTGTGTCTCTGTACTATCTTAAAGAAAAGCTTGAATGC	828
Qy	864	GAGAAATATGTCTCAACCCGACCTTCACTGTGTAAAGCTCTCAGAACCCAGGACTTACA	923
Db	829	ACGAAATGTGTCTTACCCAGACTTGAAGATGTATTAAGGCACTGAGAGCTCAGGACACACA	888
Qy	924	GTAATATTAACCCCTGTGTATGTCTTGGGCTTGGCTGTGATGCTTCCCTGTGTGTC	983
Db	889	GTCGTGTGCCCCGTGTATTTCTTGTGTGCTTGTATCCCTCTCTTCAATGTGT	948
Qy	984	TTAGCATGTGCTTACAGCGGTGGAAGCCAAAGCTTACTCATATTTGGGGCAGTGC	1043
Db	949	TTATATGTATCCCTTACCAAGCGTGAAGTCCAAGCTTACTCATTTGTTGTGGGAAATCG	1008
Qy	1044	ACTGTGTAAAGAGGGGAGCCAGAA-----CTCTGTGTCCGGCCCCAGGCTTC	1094
Db	1009	ACACTGTAAAAAGGGGGAGCTGTGAAGAACTACTACTMAAGCCCTGTGGCCCCAAACCCA	1068
Qy	1095	AAACCCACCAACATATGTGCTTACAGTCCACCCCAAGTTCAGTCCGTCTCCATTC	1154
Db	1069	AGCTTCAATCCCATCTCCAGAGCTTCAACCCCAACCTGTGGGCTTCAAGTCCGTGCCAGTTC	1128
Qy	1155	CCTTACATCTCTGTGACCGGTCCAACTTGTGAG-----CCGTGCATCTTCCCTCC	1205
Db	1129	ACCTTCACTCCAGTCCACCTATACCCCGGTGACTGTCCCAATTTGGCGCTCCCGC	1188
Qy	1206	AGCGAGACGGCCCCCCTCATCTTAAAGGTGTGCCCCCATCTCTCCGGGGGCTTCGGGCTTC	1265
Db	1189	AGAGAGGTGGACCAACCTATACAGGGGCTGACCCCATCT-----	1229
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Db	1230	-----TGGCAGACCTTC	1242
Qy	1326	GCTTCCACCACTTGTGACCCCCAGTTTAAAGTGGAAAGCCAGTCCCAAGCCCTCC	1385
Db	1243	GCTTCCGAGCCCATCCCAACCCCTTCAAGATGGGAGAGAACAGGCCACAC--AGCCA	1299
Qy	1386	GATCAGCTCGCGGATGCGGAGCCCGCGAGCCCTGTACGGGGTGTGTGAAGGGGCTGTGCCCG	1444
Db	1300	CAGAGCTTAGACACTGATGATCCCGCGAGCGTGTACGCCGTGTGTGAAACCTGTGCCCG	1355
Qy	1446	TCGCGCTGGAAGAGTGTGTGCGGCGGCTGGGACTGAGCGAGCAAGATGTGAGCGCTG	1504
Db	1360	TTGCGCTGGAAGAAATTGTCGTGGGCGCTTACGGGCTGAGGACCAAGATCATCATGCGCTG	1413
Qy	1506	GAGCTGTGAAGAGGGGCGCACTGTGGCGAGGGGCACTACAGATCTGTGGCGGCTGTGGCG	1566
Db	1420	GAGCTGTCAAGAGGGGCGTGTCTGTGCGAGGGGCGCACTACAGATGTGTGGCGACTGTGAGG	1477

Qy 1566 GGGGAGACGCGCGCCGCGAGAGCCACGCTGAGCTGTGGAGCGCGCTGCAGGAGCATG 1625

Db 1480 CGGGGACGCGCGCGCGAGGCCACGCTGAGCTGTGGAGCGCGCTGCAGGAGCATG 1539

Qy 1626 GACCTGCTGGGTTGCTCGAAAAATAGAGAGCGCTGGGTGAGCGCGCCGCGCTCGCG 1685

Db 1540 GACCTGCTGGGCTGCTCGAGAGACATGAGGAGGCGCTTTGGCGGCGCGCGCTCCCG 1599

Qy 1686 TCCGAGCCCGCGCTTCTCTGTGAGAGCCCGCGCTTCG 1724

Db 1600 CCGCGGCGCACTTCTTCAGATGAGGCGCGCGCTTCG 1638

RESULT 8
US-08-050-319B-24

Sequence 24, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M Feldmann, P.W. Gray,
APPLICANT: M J C. Turner, F M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:

ADDRESS: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:

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?      LENGTH: 2062 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: double
?      TOPOLOGY: linear
?      MOLECULE TYPE: cDNA to mRNA
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 155..1519
?
US-08-050-319B-24

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Query Match	29.5%	Score 718.6	DB 1	Length 2082
Best Local Similarity	69.4%	Pred. No. 3.7e-148		
Matches 1123	Conservative	0	Mismatches 144	Indels 92
			Gaps	7
QY	148	TCGCCCGCCCGCAGTCAACCTCCACATCCCGACCCGAGGCGCGGCTCCACATGGACA	207	
Db	9	TCTCTATGCCCGAGTCTCAACCTTCACTGTGTACCCCAAGGACATTGGACGTCCTCGAGC	68	
QY	208	TACGCGAGGACCGTGTGCTGCTCACTGTGCGGCGCGCCACTGTGCC-CAGCCTGATGGG	266	
Db	69	AGACCGAGTCCCGGCGAAGCCCGACATGCCCTCGCCACACATGCGCTGAGCCCAATGGG	128	
QY	267	GGATTGAGAGGCGACACGTGCGCGGACATGGGCTCTCCACCGTCTGGGCTGTGCTGTG	326	
Db	129	GGAGTGAAGGCGCATAGCTGTCTGG-CATGGGCTCTTCCACCGTGTCTACCTGCGTGTG	187	

Query Match 29.5%; Score 718.6; DB 2; Length 2062;
 Best Local Similarity 69.4%; Pred. No. 3,7e-148;
 Matches 1123; Conservative 0; Mismatches 404; Indels 92; Gaps 7;

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Qy 148 TGTCCCGCCCGGCTCTCAACCTCCCACTCCCGAACCCGAGCCCGGCTCCACTGGCA 207
Db 9 TCTCTATGCGCGAGCTCAACCTCAACTCACTCAACCCCAAGCACTTGAAGCTCTGAC 68

Qy 208 TAGCGAGAGACCGCTGTCTGTCACTGTGCGGGGCGCCCACTGCC-C-CAGCCCTGATGG 266
Db 69 AGACCGAGTCCCGGGAGAGCCCGACACTGCGCTGCGACACTGCCCTGAGCGCCAAATGG 128

Qy 267 GATTTGAGAGCCCAAGCTGCGCGGACATGGGCTCCCACTGCTGCTGCTGCTG 326
Db 129 GAGGTGAGAGGCGCTAGCTGTCTGG-CATGGGCTCTTCAACCGGCTGACTGCTGCTG 187

Qy 327 CCACTGTGCTTCCAGCTCTGTGTGGAGATGTATACCCCGAGGGGTTCAGGGGCTGTC 386
Db 188 CCGCTGTGCTCTCGAGCTGTGTGGAGATATACCTCTCAGGGGTATATGGACTGTC 247

Qy 387 CCTCAACCCCGGGGAGCTGAGAGAGAGAGAGTCCCTGTCCCAAGGAAATATATACAC 446
Db 248 CTTACCTTAGGGGAGAGAGAGAGATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 307

Qy 447 CCGCAAAATAGCACTTGTGTGACCAAGTGCACAAAGGTACTATCTGTATGATGAC 506
Db 308 CTTCAAAATATATGATTTGTGTATCCAAAGTGCACAAAGGTACTATCTGTATGATGAC 367

Qy 507 TGTTCGGGTCCAGGGGAGAGACAGGACTGCGAGGTGTGTGTGTGTGTGTGTGTGTGTGT 566
Db 368 TGTTCAGGGGCGGGGAGAGATGAGTGTGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGT 427

Qy 567 TTGAGAGAACCTCTCAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 626
Db 428 TCAAGAAACCACTCAGAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 487

Qy 627 GTGAGATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 686
Db 488 GTGAGATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 547

Qy 687 TACCGGGAATCTGGGGTGAATCTGGCTTCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 746
Db 548 TACCGGGAATCTGGGGTGAATCTGGCTTCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 607

Qy 747 GGCACAGTGAATATCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 806
Db 608 GGCACAGTGAATATCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667

Qy 807 TTTCTTTCTTAAAGCGCGCAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 863
Db 668 TTTCTTTCTTAAAGCGCGCAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 727

Qy 864 GAGAGATTTATCCAAACCGGAGCTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 923
Db 728 ACAGAGTGTGTCTTCAACCGGAGCTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 787

Qy 924 GTACTATTAACCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 983
Db 788 GTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 847

Qy 984 TTAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1043
Db 848 TTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907

Qy 1044 ACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1094
Db 908 ACACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967

Qy 1095 AACCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1154
Db 968 AGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1027

Qy 1155 CCTTACATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1205
  
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Db 1028 ACCCTTACCTTCAAGCTTCAACCTATATACCCCGGAGCTGTCCCAACTTTGTGGCTCCCG 1087
Qy 1206 AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1265
Db 1088 AGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1128
Qy 1266 ACCCAGCTTGTATCCCGGGGCTTCCGCTTCAACCACTGTGTATCCCTGGGGCTTCCG 1325
Db 1129 -----TGCAGACGCTTC 1141

Qy 1326 GCTTCAACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1385
Db 1142 GCTTCAACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1198

Qy 1386 GATCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1445
Db 1199 CAGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1258

Qy 1446 TCGCGCTGAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1505
Db 1259 TGTGCTGTGAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1318

Qy 1506 GAGCTGTGAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1565
Db 1319 GAGCTGTGAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1378

Qy 1566 CCGGCGACCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1625
Db 1379 CCGGCGACCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438

Qy 1626 GACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1685
Db 1439 GACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1498

Qy 1686 TCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1744
Db 1499 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1557

RESULT 10
US-08-406-824A-3
; Sequence 3, Application US/08406824A
; Patent No. 6541610
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
; FILE REFERENCE: A-71592
; CURRENT APPLICATION NUMBER: US/08/406,824A
; PRIOR FILING DATE: 1995-03-20
; PRIOR APPLICATION NUMBER: US 08/255,849
; PRIOR FILING DATE: 1994-06-08
; PRIOR APPLICATION NUMBER: US 07/860,710
; PRIOR FILING DATE: 1992-03-30
; PRIOR APPLICATION NUMBER: US 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: US 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: US 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: US 07/403,241
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
; OTHER INFORMATION:
; FEATURE:
  
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; INFORMATION FOR SEQ ID NO: 10:
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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1956 base pairs
;   TYPE: nucleic acid
;   STRAIGHTNESS: single
;   TOPOLOGY: linear
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US-08-762-308-10

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Query Match	22.7%	Score 554;	DB 2;	Length 1956;
Best Local Similarity	64.3%;	Pred. No. 3.5e-12;		
Matches 962;	Conservative	0;	Mismatches 465;	Indels 69;
				Gaps 6

Oy	233	TGTGGCGGGGGCGGCACTGCGCCGACCCCTGAAATGGGGAGATTAGAGAGAGCCACAGCTGGCCGGA	292
Db	35	TGTAATATTGCTGGCCCTGTGCCAGCCCCCAATGGGGAGATGAGAGGCCACTGCGCGGCCGA	94
Oy	293	CATGGAGCTCTCCCAACCCGTCCTGGACCTGCTCTGCACTGGTGTCTTCAGCTCTGTGTGGC	352
Db	95	CATGGAGTCTCCCAACCCGTCCTGGACCTGCTCTGCACTGGTGTCTTCAGCTCTGTGTGAT	154
Oy	353	AGATGTGTACCCCGCAGAGGGATTCAAGGGCTGTGCTCCCTCACCCCGGGAGCCTGGAGAAAG	412
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Oy	413	AGAAATGCCCTGTGCTCCCAAGAGAAATATTAACCCCGGAAATATGACACATTTGCTGCAC	472
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Oy	473	CAAGTGCACAAAGGTACTTATCTGTACAATGACTGTCCGGGTCCAGGGCAGACACGGA	532
Db	275	CAAGTGCACAAAGGAACCTACTTGTGTAGTGTGACTGTCCGAGCCCAAGGCGGGATACGT	334
Oy	533	CTGCAGAGGTGTGTGCCCTTGGCACCTACATGCTCCTTGGAGAACATCTCAGACATGCT	592
Db	335	CTGCAGAGGATGTGTAAGAGGACACTTTACGGCTTCCAGCAATTAACCTCAGGCAGTGCT	394
Oy	593	GAGCTGTCCACAGGTGCCGGGACGAATTTTCAGGTGGAAGATTTCGCTTGTGTAGTGA	652
Db	395	CAGTTGCAGACATGTTCGGAAGAAATGTCCAGGTGGAAGATCTCTCTTGCACAACTGA	454
Oy	653	CCGGGACACTGTGTGTCGGCTCAGAGAAACACAGTACGGGAATATCTGGGTGAACTGG	712
Db	455	CAAGGACACGGTGTGTGTGCTGTAGAGAACCAAGTTCGAAGCTACCTGATGAGACACA	514
Oy	713	CTTCGGTGTGTGAACCTGCAGCCTCTGTCCAAATGACACAGTGAATATCCCTGACAGA	772
Db	515	CTTCAGTGGGTGTGACTGCAGCCCCCTGTTCAAACGGCACCGTGAACATCCCTGTAAGA	574
Oy	773	GAGACAGACACACATCTGCGCACTGCCATATATGGGCTTTCTTTAAAGCGCCAAAGTCAT	832
Db	575	GACTCAGAACACCGTGTGTACTGTCCATGCACAGAGGTTCTTTCTGAGAGAAAGTGAATGCT	634
Oy	833	CTCCTGTATGATTTGTAGAACA---AGAGTGCAGAGAAAGTTATGTCCAACCCGAC---	886
Db	635	CCCTTGCAGCCACTGCAGAGAAATATGAGAGTGTATGAAATTTGTCTTACTCTCTCCGCT	694
Oy	887	TTCAACTGTGTAAAGACTCTCAGAGCCACAGGACCTACAGTACTATTAACCTCGTGATTTGT	946
Db	695	TGCAAATGTACAACAAACCCCGAGGACTCAGGTACTCGGGTGTGTTGCCCTGTATATTT	754
Oy	947	CTTGGGGCTTTTGCTGCGCATCTTGGCCTCTGTGCTCTTAGCATGTGGCTACACGGGTG	1006
Db	755	GCTAGAGTCTTTGCCCTTATCTTATCTTATCTTACATGATTAAATGTGCGATATCCCGGTG	814
Oy	1007	GAAGGCCAAGCTCTACTCATCATTTTGGGGGAGTGCAGCTGTGTAAAGAGGGGGAGCC	1066
Db	815	GAGGCCCAAGTCTACTCATATTTTGAAGGATCCGCTGCTGTCAAGAGAGAGAAAGC	874
Oy	1067	---AGAACTCTTGATCCCGGCCCAAGGCTTCAACCCCAACACACATCTGTCAAGTCT	1123
Db	875	TGGAAGAGCCCTTAATCTCAGAGCCCTCCGCCACCTTACAGCCCACTCCGGCTTCAACCC	934
Oy	1124	CACCCCAAGTTCAGTCTGTCTTCATTTCCCTTACATCTCTGTGACCGGTCCAACCT	1183

Db	935	CACCTCTGGGCTTCAGCAACCCCGAGCTTTACTTCTCTCGTCTCCAGTAACCCCGCATCAGCCC	994
QY	1184	CGGAGCCGCTGCATCTCTCCTCACGGACGAGCGGCCCGCCCATCTTAAAGCTGGCCCCAT	1243
Db	995	CATCTTGGGTCTTAGTAATCTGGCACTTTCATGACCACCTGTCAGTAGAGGTAGTCCCAACCCA	1054
QY	1244.	CTCTCCGGGGGCTCCGGAGCTCCACCCACACCTCTGTATACCCCGGGGCTCTCGAGCTCCACCCA	1303
Db	1055	GGGAGCTGACCCCTCTGTCTTACGAATACCTGTCTCGTCCGTGCAGCCCC-----	1102
QY	1304	CTTCTGTACCCCGGGGCTCTCGGCTTCACCCACCTCTGCACCCAGCTTCAAGAGTGGGA	1363
Db	1103	-----CACTCTGTCTTCAGAAATGGGA	1123
QY	1364	AGCCAGGGCCCCCAGCCGCCCCCATCACTCTGGGAGATCGGAGACCCCGCGACCCCTGTACGC	1423
Db	1124	AGACTCTGAGCC-----ACCAGCAACCTCTTCGACAAATGCACACCTTGGATTCGTATGC	1177
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Db	1178	TGTGTGGATGGCGCTGCTCCAGCGCGCTGGAAAGAGTTCAATGGCTTTCATGGGGCTCAG	1237
QY	1484	CGAGCAGAGATCGAGCGGCTGGAGCTGGAGAAATGGGCGCCCACTTGGCGCAGGCGCCACTA	1543
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QY	1604	GGGCGCGCTGCTCAGGGACATGACCTTGTCTGGGTTGCTTGGAAAAATAGAGAGGCGCT	1663
Db	1358	GGGCGCTGTGCTTTCAAAGATGAACCTTGGCGGCTGCTCGAGAAATATCTTCGAGGCTCT	1417
QY	1664	GGGTGGCGCGCGCGGCTTGGCGCTCGAGAGCCCGGCTTCTCTGGTGAAGAGCCCGGCGCC	1719
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RESULT 12
US-09-513-007-3
; Sequence 3, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehli, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS
; TITLE OF INVENTION: AID METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBERS: US/09/513,007
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/1122,156
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO: 3
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(543)
US-09-513-007-3

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Query Match      22.3%  Score 543;  DB 4; Length 543;
Best Local Similarity 100.0%;  Pred. No. 6.5e-110;
Matches 543;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0

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Db      1 CTGTCCTCCACCCCGGGGACCTGGAGAGAGAGAGTCCCTGTCCTCCCAAGAAAATAT 60
Qy      441 AACCAACCCCAAAATATGACACATTTGCTGACCAAGTGCACAAAGTAATCTTATCTTAC 500
Db      61 AACCAACCCCAAAATATGACACATTTGCTGACCAAGTGCACAAAGTAATCTTATCTTAC 120
Qy      501 AATGACTGTCGGGTCGACGGGCGAGACAGGACTGAGGAGTGTGTCCTGCGACCTTAC 560
Db      121 AATGACTGTCGGGTCGACGGGCGAGACAGGACTGAGGAGTGTGTCCTGCGACCTTAC 180
Qy      561 ACTGCTTGGAGAACCATCTTCAAGAGATGCTTGAAGTCTGAGTGCAGGTCGCGGAGCAAAATG 620
Db      181 ACTGCTTGGAGAACCATCTTCAAGAGATGCTTGAAGTCTGAGTGCAGGTCGCGGAGCAAAATG 240
Qy      621 TTCCAGTGGAGATTTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 680
Db      241 TTCCAGTGGAGATTTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Qy      681 AACCAATCCCGGAAATATCTGGGGTAAACTGGCTTCCGGTGTGTGAACCTGACGCTTGT 740
Db      301 AACCAATCCCGGAAATATCTGGGGTAAACTGGCTTCCGGTGTGTGAACCTGACGCTTGT 360
Qy      741 CCCAATGCGACAGTGAATATCTTCCCTGCGAGAGAGACAGACAGACATCTGCCACTGCCAT 800
Db      361 CCCAATGCGACAGTGAATATCTTCCCTGCGAGAGAGACAGACAGACATCTGCCACTGCCAT 420
Qy      801 ATGGCTTCTTTCTTAAAGGGCGCAAGTGCATCTCTGATGATTTGAAGAACAAAGAG 860
Db      421 ATGGCTTCTTTCTTAAAGGGCGCAAGTGCATCTCTGATGATTTGAAGAACAAAGAG 480
Qy      861 TCGGAGAGTATATGTCCAACCCGACCTTCACTGTGTAAAGACTCTCAGAGCCAGGACT 920
Db      481 TCGGAGAGTATATGTCCAACCCGACCTTCACTGTGTAAAGACTCTCAGAGCCAGGACT 540
Qy      921 ACA 923
Db      541 ACA 543

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RESULT 13

US-08-286-740-2

Sequence 2, Application US/08286740

Patent No. 5561053

GENERAL INFORMATION:

APPLICANT: Crowley, Craig W.

TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,740

FILING DATE: 05-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 798

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

```

; TELFAX: 415/952-9881
;
; TELE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6889 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-286-740-2

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Query Match      16.0%; Score 389.8; DB 1; Length 6889;
Best Local Similarity 76.6%; Pred. No. 3.9e-76;
Matches 491; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

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Qy      287 GCCGACATGAGGCTCCCAACCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 346
Db      1598 GTCTGACATGAGGCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 1657
Qy      347 GTTGGCAGATGTATACCCCGAGGGGCTTCAAGGGCTGTCCCTTCAACCCCGGAGACTTGA 406
Db      1658 GTTGGCAGATGTATACCCCGAGGGGCTTATGAGTGTCTCTCACTAGGGGAGACAGGA 1717
Qy      407 GAAGAGAGAGATCCCTGTCCCAAGAAATATTAACACCCGCAAAATAGACCATTTG 466
Db      1718 GAAGAGAGATGTATGCTGTCTCCCAAGAAATATTAACACCCCTCAAAATATGATTTG 1777
Qy      467 CTGACCAAGTCCCAAAAGTATCTTGTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
Db      1778 CTGACCAAGTCCCAAAAGTATCTTGTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1837
Qy      527 CACGAGCTGACGGGTTGTGCTCCCTGGACCTTACAGCTGCTTGGAGAACATCTCAGAG 586
Db      1838 TACGAGCTGACGGGTTGTGAGAGGCTCTTCAAGCTTCAAGAAACCACTTACAGCA 1897
Qy      587 ATGCTTGAAGTCTTCAAGTGTCCGAGAGCAAAATGTCAGAGTGAATTTGCTGCTGTGT 646
Db      1898 ATGCTTGAAGTCTTCAAGTGTCCGAGAGCAAAATGTCAGAGTGAATTTGCTGCTGTGT 1957
Qy      647 AGTGAACCGGAGACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
Db      1958 AGTGAACCGGAGACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2017
Qy      707 AACTGCTTCCGAGTGTGAACTGACAGCTGTCTGCTCCCAATGAGCAAGTGAATATCCCTG 766
Db      2018 AACTGCTTCCGAGTGTGAACTGACAGCTGTCTGCTCCCAATGAGCAAGTGAATATCCCTG 2077
Qy      767 CCAGAGAGACAGACACATCTGCACTGCAATATGAGGCTTTCTTTTAAAGGCGGCA 826
Db      2078 CCAGAGAGACAGACACATCTGCACTGCAATATGAGGCTTTCTTTTAAAGGCGGCA 883
Qy      827 GTGCATCTCCGTGATGATTTGAAGAA---CAAGAGTGGAGAAATATGTCACACCG 883
Db      2138 GTGTGCTCTCTGATGATGATTTGAAGAAAGCTGGAATGACAGAAATGTCCTTACCA 2197
Qy      884 ACCTTCACTGTATTAAGACTCTCAGAGCCAGGACCTACAG 924
Db      2198 GATTGAAGATTTAAGGCACTAGAGCTCAGGACACACAG 2238

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RESULT 14

PCT-US95-09576-2

Sequence 2, Application PC/TUS9509576

GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.

TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA


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Db 1174 CTGCAGGAGATGTGAGAGGGGCTCTTCAACCGCTTCAGAAAACACCTCAGACACTGCCT 1233
Oy 593 GAGCTGCTCCAGGTCCGGAGCGAATGTTCCAGGTGAGATTTGCGCTTGTGTAGTGA 652
Db 1234 CAGCTGCTCCAAATGCGAAAGGAATGGTCAGGTGAGATCTCTTGTGCACAGTGA 1293
Oy 653 CCGGACACTGTGTGCGGCTGCGAGGAACAGATACCGGGAATCTGGGGTGAACCTG 712
Db 1294 CCGGACACTGTGTGCGGCTGCGAGGAACAGATACCGGCAATTGAGAGTGAACCT 1353
Oy 713 CTTCGGGTGCTGAACCTGAGCCTCTGTGCCAATGGCACAGTGAATATCCCTGCCAGGA 772
Db 1354 TTTCAGATGCTTCAATTGACAGCCTCTGCTCAATGGGACCGTGCACCTCTGCGCAGGA 1413
Oy 773 GAGACAGACACCATCTGCACTGACCATATGGCTTCTTTAAAGGCGCAAGTCAT 832
Db 1414 GAAACGAAACACCGTGTGCACTGCCCATGCAAGGTTCTTTAAGAGAAACGAGTGTGT 1473
Oy 833 CTCTGTGATGATTTGAAGAA---CAAGGAGTGCAGAAATTATGTCCAAACCGACCTTC 889
Db 1474 CTCTGTGATGATGTAAGAAAGCCTGAGATGCAAGAAATTGTGTCTAACCCAGATTGA 1533
Oy 890 AACTGTAAAGACTCTCAGGACCCAGGCACTACAG 924
Db 1534 GAATGTAAAGGCACTGAGGACTCAGGCACACAG 1568
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Search completed: September 15, 2003, 07:52:08
Job time : 139 secs

Qy	121	GGGTTGAGGCTCTCCGGATTTGGGCTGTCTCCCGCCCCAGCTCTCAACCTTCACATCCCC	180
Dp	121	GGGTTGAGGCTCTCCGGATTTGGGCTGTCTCTCCCGCCCCAGCTCTCAACCTTCACATCCCC	180
Qy	181	GACCCGAGGCCCGGGCTCCACTGTGGCATACGCGAGAACCGTGTTCCTGTCACTGTCCGCG	240
Dp	181	GACCCGAGGCCCGGGCTCCACTGTGGCATACGCGAGAACCGTGTTCCTGTCACTGTCCGCG	240
Qy	241	GCCGCGACTGCCCCCAGCCCTTGATGGGGGATTGAGAGGCCACAGCTGGCCCGACATGGGCC	300
Dp	241	GCCGCGACTGCCCCCAGCCCTTGATGGGGGATTGAGAGGGCCACAGCTGGCCCGGACATGGGCC	300
Qy	301	TCCCCACCGGTCCCTGGACCTGTGTGCGACACTGGTACTTTCAGAGCTCTGTTGGCAGATGTGT	360
Dp	301	TCCCCACCGGTCCCTGGACCTGTGTGCGACACTGGTACTTTCAGAGCTCTGTTGGCAGATGTGT	360
Qy	361	ACCCGCGAGGGGTTCAGGGGGCTGTGCTCCATCCCCGGGGACCTTGAGAGAGAGAGATC	420
Dp	361	ACCCGCGAGGGGTTCAGGGGGCTGTGCTCCATCCCCGGGGACCTTGAGAGAGAGAGATC	420
Qy	421	CCTGTGCCCAAGGAAAAATATACCCGCGCAAAATAGACATTTGCTGTGCACAAATGCC	480
Dp	421	CCTGTGCCCAAGGAAAAATATACCCGCGCAAAATAGACATTTGCTGTGCACAAATGCC	480
Qy	481	ACAAAGGTACTCTATCTGTACATGACTGTCCGGGTCAAGGGGAGACACGACTGACAGG	540
Dp	481	ACAAAGGTACTCTATCTGTACATGACTGTCCGGGTCAAGGGGAGACACGACTGACAGG	540
Qy	541	TGTGTGCCCCCTGGGACCTTACACTGCTTTGGGAAACACTTCAAGAGATGCTGTAGCTCT	600
Dp	541	TGTGTGCCCCCTGGGACCTTACACTGCTTTGGGAAACACTTCAAGAGATGCTGTAGCTCT	600
Qy	601	CCAGGTGCCGGAGCGAAATGTTTCCAGGTGAGATTTCCGCTTGTGTAGTGGACCGGAGCA	660
Dp	601	CCAGGTGCCGGAGCGAAATGTTTCCAGGTGAGATTTCCGCTTGTGTAGTGGACCGGAGCA	660
Qy	661	CTGTGTGGGCTGCGAGAAAGAACCAATACCGGGAAATCTGGGGTGTAAACTGGCTTCCGCT	720
Dp	661	CTGTGTGGGCTGCGAGAAAGAACCAATACCGGGAAATCTGGGGTGTAAACTGGCTTCCGCT	720
Qy	721	GTCGTAACTGAGAGCTCTGTCCCAATGGCAGAGTAATCCCTGCCAGAGAGAGACAG	780
Dp	721	GTCGTAACTGAGAGCTCTGTCCCAATGGCAGAGTAATCCCTGCCAGAGAGAGACAG	780
Qy	781	ACACCATCTGCGCATGTGCCATATGGGCTTCTTTTAAAGGGGCCAGTGCATCTCTGTCT	840
Dp	781	ACACCATCTGCGCATGTGCCATATGGGCTTCTTTTAAAGGGGCCAGTGCATCTCTGTCT	840
Qy	841	ATGATTGTGAACCAAGAGATGCGAGAGTTATGTCAAACCGCACTTCMACTGGTAAG	900
Dp	841	ATGATTGTGAACCAAGAGATGCGAGAGTTATGTCAAACCGCACTTCMACTGGTAAG	900
Qy	901	ACTCTCAGGACCCAGGCACTACAGTACTAATACCCTGTGTATGTTCTTCGGGCTTTTGC	960
Dp	901	ACTCTCAGGACCCAGGCACTACAGTACTAATACCCTGTGTATGTTCTTCGGGCTTTTGC	960
Qy	961	TGGCATCCTTGGCCCTGTGTGCTTATAGATGTGTCACACGCGTGGAGAGCCCAAGCTCT	1020
Dp	961	TGGCATCCTTGGCCCTGTGTGCTTATAGATGTGTCACACGCGTGGAGAGCCCAAGCTCT	1020
Qy	1021	ACTGCATCATTTTGGCGGAGTGCATCTGTGTAAAGAGAGGGGAGCCCAAACTCTGTGTCT	1080
Dp	1021	ACTGCATCATTTTGGCGGAGTGCATCTGTGTAAAGAGGGGAGCCCAAACTCTGTGTCT	1080
Qy	1081	CGGCCCCCAGGCTTCAACCCCAACCAACCACTGTGTTCACTCCACCCCAAGTTTCAAGTC	1140
Dp	1081	CGGCCCCCAGGCTTCAACCCCAACCAACCACTGTGTTCACTCCACCCCAAGTTTCAAGTC	1140
Qy	1141	CTGTCTCATTTCCCTTTACATCTCTGTGACCGGTCAACCTTGGAGACCGTGCATCTTC	1200
Dp	1141	CTGTCTCATTTCCCTTTACATCTCTGTGACCGGTCAACCTTGGAGACCGTGCATCTTC	1200
Qy	1201	CTTCACAGAGACGAGCCCGCCCCCATCTTAAAGCTGCGCCCATCTCCCGAGGCTCTCCG	1260

Db	1201	CTTCAAGGAGACGGGCCCCCACTAAAGGCTGGCCCCATCTCCCGGGCTCCGG	1260
Oy	1261	CTTCAACCCACTCTGTACCCCGGGGCTCCGGGCTCAACCCACTCTGTACCCGGGG	1320
Db	1261	CCTCAACCCACTCTGTACCCCGGGGCTCCGGGCTCAACCCACTCTGTACCCCGGGG	1320
Oy	1321	CTCCGGCTCTCAACCCACTCTGTACCCCACTTCAAGATGGAGGCCAGCCCCCAAGC	1380
Db	1321	CTCCGGCTCTCAACCCACTCTGTACCCCACTTCAAGATGGAGGCCAGCCCCCAAGC	1380
Oy	1381	CCCCGGATCAGCTCGCGATGCGACCCCGCGACCCCTGTACCGCGGTGTGAACGGCGTGC	1440
Db	1381	CCCCGGATCAGCTCGCGATGCGACCCCGCGACCCCTGTACCGCGGTGTGAACGGCGTGC	1440
Oy	1441	CCCCCTCGGCTTGAAGAGATTGTGCGCGGCTGGGACTGAGCGAGCAAGATCGAGC	1500
Db	1441	CCCCCTCGGCTTGAAGAGATTGTGCGCGGCTGGGACTGAGCGAGCAAGATCGAGC	1500
Oy	1501	GGCTGGAGCTTGAAGAAACGGGGCCCACTGCGGAGGCGCGAGTCAACATGCTGTGGCGCT	1560
Db	1501	GGCTGGAGCTTGAAGAAACGGGGCCCACTGCGGAGGCGCGAGTCAACATGCTGTGGCGCT	1560
Oy	1561	GGCGGCGGCGACAGCGCCCGCGCGAGGCGACGCTGAGGCTGTGGCCGCGTCTCAAGG	1620
Db	1561	GGCGGCGGCGACAGCGCCCGCGCGAGGCGACGCTGAGGCTGTGGCCGCGTCTCAAGG	1620
Oy	1621	ACATGGACTCTGCTGGGTTGCTGTGAAACATAGAGAGGCGCTGGTGGCGCGCCCGCC	1680
Db	1621	ACATGGACTCTGCTGGGTTGCTGTGAAACATAGAGAGGCGCTGGTGGCGCGCCCGCC	1680
Oy	1681	TGCGCTCCGAGGCCCCGCTTCTCTGGTGAAGCCCCCGCTCGACTGCGGGCTCCCGG	1740
Db	1681	TGCGCTCCGAGGCCCCGCTTCTCTGGTGAAGCCCCCGCTCGACTGCGGGCTCCCGG	1740
Oy	1741	CCCTGCAAGACGGCTGCTTCTCTGTGCGAGGACCCGGAAAGATCTGCGAGATGCC	1800
Db	1741	CCCTGCAAGACGGCTGCTTCTCTGTGCGAGGACCCGGAAAGATCTGCGAGATGCC	1800
Oy	1801	TGTGACCCCTCGT	1860
Db	1801	TGTGACCCCTCGT	1860
Oy	1861	GATCTGGCAGCCACTGACCTGCTGCTACTCACTGATCATAGCTTTTCTCAGCTGCC	1920
Db	1861	GATCTGGCAGCCACTGACCTGCTGCTACTCACTGATCATAGCTTTTCTCAGCTGCC	1920
Oy	1921	TGAGT	1980
Db	1921	TGAGT	1980
Oy	1981	TGTGCGTCTGT	2040
Db	1981	TGTGCGTCTGT	2040
Oy	2041	CCAAGGCACTGTTGCGAAGATGAGAGGGCGCTGCTTATGCTGTGTGTGTGTGTGTGTGT	2100
Db	2041	CCAAGGCACTGTTGCGAAGATGAGAGGGCGCTGCTTATGCTGTGTGTGTGTGTGTGTGT	2100
Oy	2101	GAGAACTCAGCAAGGCGACTTGGGAAACCTAGTGGTCCCTGAGCGCGGTTTGCAGTAG	2160
Db	2101	GAGAACTCAGCAAGGCGACTTGGGAAACCTAGTGGTCCCTGAGCGCGGTTTGCAGTAG	2160
Oy	2161	ATAGGCCATCTTTGTATCACTCTGTGCATCTCACTCATCTGTATCACTATATAGAAA	2220
Db	2161	ATAGGCCATCTTTGTATCACTCTGTGCATCTCACTCATCTGTATCACTATATAGAAA	2220
Oy	2221	CTTGTGTGCGGCTGTGAGCAAGCTGAACTGTCTCCAGGCAAGGAGGAGACACAGAAAAA	2280
Db	2221	CTTGTGTGCGGCTGTGAGCAAGCTGAACTGTCTCCAGGCAAGGAGGAGACACAGAAAAA	2280
Oy	2281	TGGGGCTTCCAAAGGAGCTAGCTGTTCAGTTCACTTCACTGCTGCTGCTGCTGCTGCTGCT	2340

Db 1210 CCATCCCCAACCCCTTCAGAAAGTGGAGAGACAGCCCAACA---AGCCACAGAGCTTAG 1266
Qy 1396 CGGATGCCGACCCCGGACCCCTGTACGCGGTGTGAGAGCGCGTCCCGCTGCGCTGGA 1455
Db 1267 ACACTGATGAGACCCCGGACCGCTGTACCGCGGTGTGAGAGAGCTGCGCCCGTTGGCGTGA 1326
Qy 1456 AGGAGTTGTGCGCGCGCTGAGACTGAGCCGAGCAGAGATGAGCGGTGGAGCTGAGGA 1515
Db 1327 AGGAATTCGTGCGCGCTGAGCGCTGAGCCAGCAGAGATGATCGGTGAGCTGAGGA 1386
Qy 1516 ACGGGCGCCACCTCGCGAGGCGGAGTACAGATGTGAGCGCGCTGCGCGGCGGCGACGC 1575
Db 1387 ACGGGCGCTGCTCGCGAGGCGGAGTACAGATGTGAGCGAGCTTGGAGGCGGCGACGC 1446
Qy 1576 CGCGCGCGGAGGCGGAGTGTGAGCGCGCTGCGCGCTGAGGAGACATGAGCTGTGCG 1635
Db 1447 CGCGGCGCGAGGCGGAGTGTGAGCGCGCTGCGCGCTGAGGAGACATGAGCTGTGCG 1566
Qy 1636 GTTGCCTGGAAAAATATAGAGAGGCGTGGGTGGCGCGCGCGCTGCGCTGCGAGCCGC 1695
Db 1507 GCTGCTCGAGAGCATGAGAGAGCGCTTGTGCGCGCGCGCGCGCTGCGCGCGCGCA 1566
Qy 1696 GCCTTCTGTGTAAGCGCGCGCGCTGCG 1724
Db 1567 GTCTTCTGAGTGAAGCTGCGCGCGCTGCG 1595

RESULT 4

US-09-999-429A-26
Sequence 26: Application US/09899429A
Patent No. US20020169118A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hummel, Adolph
APPLICANT: Mauser-Fogy, Ingrid
APPLICANT: Stralowa, Christian
TITLE OR INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
FILE OR INVENTION: Them
FILE REFERENCE: 98-385-J
CURRENT APPLICATION NUMBER: US/09/899,429A
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/792,356
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 2141
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
NAME/KEY: CDS
LOCATION: (213)..(1577)
US-09-999-429A-26

Query Match 30.2%; Score 737, DB 10; Length 2141;
Best Local Similarity 69.9%; Pred. No. 8.2e-177;
Matches 1152; Conservative 1; Mismatches 401; Indels 95; Gaps 8;

Qy 101 GGCGGAGGCGGCTGCTTCCGGGTTTGAAGTCTCCGATTTGGGCTGCG---TCCCGCC 157
Db 17 GGCTCCAGTTTGGGCTTTGGGGTTTCAAGATCACTGGGACCAAGGCGGTATCTCTATGCC 76

Qy 158 CCACTCTCAACCTCTCACTCCCGAGCCCGAGCCCGGCTTCACCTGGGCATATCCGAGGA 217
Db 77 CGAGTCTCAACCTCTCACTGTCACCCCAAGGCACTTGGGAGCTCTGGAACAGACCGAGTCC 136
Qy 218 CCGTGTGTCTGCTCACTGTGCGGAGCGGCACTGCGCC--AGCTCGATGTGGGGATTTGAGAG 276
Db 137 CCGGAGAGCCCGAGCACTGCGCGTGCACACTGCTCCGAGGCCCAKATGGGGAGTGAAG 196
Qy 277 GCGACAGCTGGCCGGAATGAGGCTCCCGACCCGCTGCGCTGCTGCTGCTGCTGCTGCTG 336
Db 197 GCGATAGCTGTCTG--CATGGGCTCTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 255
Qy 337 TTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAAGGGGCTGCTGCTGCTGCTG 396
Db 256 TCTGAGAGCTGTTGGTGGAAATATACCTCCAGGGGTTATTTGAGCTGTGCTTCACTAG 315
Qy 397 GGGACCTGGAGAGAGAGAGAGTCTGCTGCTCCAGAGAAATATATACCCGCAATA 456
Db 316 GGGACAGGGAGAGAGAGATGTGTGTGCTCCCAAGAGAAATATATATATATATATATAT 375
Qy 457 GCACATTTGTGTCAGCAAGTGCACAAAGGTACTTATGTATCAATGATGTGCGGGTCT 516
Db 376 ATTGATTTGTGTATCCAGATGCTCACAAGAGACTTGTATGATGATGATGATGATGATG 435
Qy 517 CAGGGCGAGACACGAGCTGAGGAGGTGTGCTCCCTGCGCACTACATGCTTGGAGAAC 576
Db 436 CGGGGAGAGATGAGGATGAGGAGGTGTGAGAGCGGCTCTTCACTGAGGCTTCAAGAAAC 495
Qy 577 ATCTCAAGATGCTGAGCTGCTGCTGAGGTGCGGGAGCAAAATTTTCCAGTGGAGATT 636
Db 496 ACCTCAGACACTGCTGCTGCTGCTCAAAATGCGCAAAATGAGTGTGAGTGTGAGTGT 555
Qy 637 GCGCTGTGTATGATGAGACGGGAGCACTGTGTGCGGCTGAGAGAGACAGTACCGGGAT 696
Db 556 CTTTTCACAGTGTGAGGAGGAGACGCTGTGTGCTGAGAGAGACAGTACCGGGAT 615
Qy 697 ACTGGGCTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756
Db 616 ATTGAGTGAAGAACTTTTCAAGTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
Qy 757 ATATCCCTGCTGAGAGAGAGACAGACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
Db 676 ACCTCTCTGCTGAG 735
Qy 817 AAGGCGCAAGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 873
Db 736 GAGAAACAGAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
Qy 874 GTCCACCCGACCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 933
Db 796 GCGTACCCGAGTGTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 855
Qy 934 CCGTGTGATGTCTTGGGCTTGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 993
Db 856 CCGTGTGATGTCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 915
Qy 994 GCTACAGCGGTGAG 1053
Db 916 GCTACAGAGGTGAG 975
Qy 1054 AAGAGGGGAGCCAGAA-----CTCCGTGCTCCGCGCCCGAGGCTTCAACCCCA 1104
Db 976 AAGAGGGGAGGCTTGAAGAGAACTACTAGTACAGCCCTGCGCCCAAGCCAGCTTCACTC 1035
Qy 1105 CCACATCTGCTTCAAGCTCAACCCCAAGTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
Db 1036 CCACTTCAAGCTTCAACCCCAAGTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1095
Qy 1165 CCGTGTGAGCGGCTCAACTTGGAG-----CGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1215
Db 1096 CAGCTTCAACTATATCCCGGAGTACTGTCCCAACTTGGAGGCTCCCGAGAGAGGTGG 1155

Oy 1216 CCCCCCATCTMAAGGCTGGGCCCCCATCTCCCGGGGCTCCGCGCTCAACCCACTCT 1275
 Db 1156 CACCACCTTATCAGAGGAGGCTGACCCCATCT----- 1186
 Oy 1276 GTACCCCCGGGCTCCGGGCTTCACCCACTCTGTACCCCGGGGCTCCGGCTTCACCC 1335
 Db 1187 -----TGGCAGACCCCTCGCTCCGAC 1209
 Oy 1336 ACCCTGTGACCCCACTTTCAGAGTGGGAGCCAGCGCCCCCAAGCCCCCATCAAGCTCG 1395
 Db 1210 CCATCCCCCAACCCCTTTCAGAGTGGGAGCAGCGCCCA--AGCCAGAGAGCTTAG 1266
 Oy 1396 CGAGTGGCCGACCCCGGACCCCTGTACCGGCTGGTGGAGCGGCTGCCCTCGCGCTGGA 1455
 Db 1267 ACATGTAGTACCCCGGACCGCTGTACCGGCTGGTGGAGAAAGTGGCCCCCTTGGCTGGA 1326
 Oy 1456 AGGAGTTGGTCCGCGGCTGGGACTGAGCGAGCAGAGATCGAGCGCTGGAGCTGAGA 1515
 Db 1327 AGGAAATTCGTGCGGCGCTTAGGGCTGAGCGACACAGATCGATCGGCTGGAGCTGAGA 1386
 Oy 1516 ACCGGGCGCACTCGCGGAGCGGAGTACAGATGCTGGCGGCTGGGCGGCGGCAAGC 1575
 Db 1387 ACCGGGCTGCTGGCGGAGCGGCAATACAGATGCTGGCGACTGGAGGCGGCGCAAGC 1446
 Oy 1576 CGCGCGCGGAGGCGGCTGAGAGCTGCTGGGCGCGGCTGCTGAGGAGCATGAGCTGCTGG 1635
 Db 1447 CGCGGCGGAGGCGGCTGAGAGCTGCTGGGCGCGGCTGCTGAGGAGCATGAGCTGCTGG 1506
 Oy 1636 GTTCCCTGGAAACATAGAGAGGCGCTGGGCTGGGCGCGGCTGCTGCTGCGAGCCCC 1695
 Db 1507 GCTCCCTGGAGAGCATGAGAGGCGCTGGGCTGGGCGCGGCTGCTGCGGCGGCGGCA 1566
 Oy 1696 GCCTTCTGTGTAAGCCCGGCGGCTGG 1724
 Db 1567 GTCTTCTGATGAGGCTGGCGGCTGCG 1595

RESULT 5

US-09-792-356-16

Sequence 16, Application US/09792356

Publication No. US20020183485A1

GENERAL INFORMATION:

APPLICANT: Hauptmann, Rudolph

APPLICANT: Himmler, Adolph

APPLICANT: Maurer-Fogy, Ingrid

APPLICANT: Stralow, Christien

TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for

FILE REFERENCE: 98,385-G

CURRENT APPLICATION NUMBER: US/09/792,356

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: 08/477,639

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/383,676

PRIOR FILING DATE: 1995-02-01

PRIOR APPLICATION NUMBER: 08/153,287

PRIOR FILING DATE: 1993-11-17

PRIOR APPLICATION NUMBER: 07/821,750

PRIOR FILING DATE: 1992-01-02

PRIOR APPLICATION NUMBER: 07/511,430

PRIOR FILING DATE: 1990-04-20

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 2141

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: CDS

LOCATION: (213) (1580)

OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in

OTHER INFORMATION: TNF-R2

US-09-792-356-16

Query Match 30.24; Score 737; DB 10; Length 2141;
 Best Local Similarity 69.94; Pred. No. 8.2e-177;
 Matches 1152; Conservative 1; Mismatches 401; Indels 95; Gaps 8;

Oy 101 GCGCGAGGGCTGCGCTTCCGGGTTTGAAGTCTCCGATTTGGGCTGTG---TCCCGCC 157
 Db 17 GCGTCAGTTCTGGCTTTGGGTTTCAAGATCAGTGGAGCCAGGCGGTGATCTATATCC 76
 Oy 158 CCAATTCACACCTTCACCTCCCGACCGGAGCCCGGCTCCACTGAGGATACCGGAGA 217
 Db 77 CGAGTCTCAACCTTCACCTTCACCGGAGGACCTTGGAGGCTCTGACAGACCGAGTTC 136
 Oy 218 CCGTGTGCTGCACTGTCCGGGCGGCACTGCCCC-AGCCGATAGGGGGAATTGAGAG 276
 Db 137 CCGGAGAGCCCGGAGACTGCGGCTGCGACACTGCGCTGAGGCCAATGGGAGTGAAG 196
 Oy 277 GCGACAGCTGGCCGAGACATGAGGCTCCCGACCGTGGCTGCTGCTGCTGCTGCTGCTG 336
 Db 197 GCGATAGCTGTCTGG-CATGGGCTTCCACCGTGGAGCTGCTGCTGCTGCTGCTGCTGCTG 255
 Oy 337 TTCAGCTCTGTTGAGATGTGTACCCCGGAGGCTTCAAGGCTGTCTCTACCCCG 396
 Db 256 TCCGTGAGCTGTGTGGGAAATATACCCCTCAGGGGTTATTGAGCTGTCTCTCACTAG 315
 Oy 397 GGGACCTGGAGAGAGAGAGAGTCCCTGTCCCGAAGGAAATATTAACACCGGAAATA 456
 Db 316 GGGACAGGAGAGAGAGATGTGTGTCCCGAAGGAAATATTAACACCTCAAAATA 375
 Oy 457 GCACCATTTGCTGACCAAGTGCACCAAGGTACCTATCTGTACAAATGACTGTCCGGTTC 516
 Db 376 ATTGATTTGCTGTACCAAGTGCACCAAGGTACCTATCTGTACAAATGACTGTCCGGTTC 435
 Oy 517 CAGGCGAGACACCGGACTGCGAGGCTGTGCTCCCTGCGACCTTACATGCTTGGAGAAC 576
 Db 436 CCGGCGAGGATACCGGACTGCGAGGCTGTGAGAGCGCTCTTCAACGCTTCAGAAACC 495
 Oy 577 ATCTCAGACATGCTGAGCTGCTCCAGAGTCCCGGAGGAAATGTTCCAGGTGAGATTT 636
 Db 496 ACCTCAGACATGCTGCTGAGCTGCTCCAAATGCTCCAAAGGAAATGAGTGAAGATCT 555
 Oy 637 GCGCTTGTAGTGAACCGGAGCACTGTGCGGCTGCGAGGAAACCAATCCGGGAT 696
 Db 556 CTTCTTGAACAGTGAACCGGAGCACCGTGTGCTGAGGAAACCAATCCGGGAT 615
 Oy 697 ACTGGGTTGAACCTGCTGCGGCTGTGAGACTGCAAGCTTGTCCCAATGGCACAGTGA 756
 Db 616 ATTGAGTGAACCACTTTCAGAGCTTCAATTCAGCTTGTCTCAATGGAGACCGTGC 675
 Oy 757 ATATCCCTGCGAGGAGAGACAGACACATCTGCCACTGCTATGAGGCTTTCTTTCTTA 816
 Db 676 ACCTTCTGCTGAGAGAGAGAGAGAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 735
 Oy 817 AAGGCGCCAGTGCATCTTCTGCTGATGATGTAAGAA---CAAGAGTGCAGAAATTAT 873
 Db 736 GAGAAACAGAGTGTCTCTGCTGATGATGTAAGAAAGCTGAGAGTGCAGAAATTAT 795
 Oy 874 GTCCACCCGACCTTCAACAGTGTAAAGCTGCGAGCCCGGAGCTACAGTACATATAC 933
 Db 796 GCGTACCCGAGTGAAGATGTAAGGAGCACTGAGAGCTGAGGACCAACAGTGTGCTG 855
 Oy 934 CCGTGTGATTTGCTTGGGCTTGGCTGAGCATCTTGCCTGTGCTGTGCTGCTGCTGCTG 993
 Db 856 CCGTGTGATTTGCTTGGGCTTGGCTGAGCATCTTGCCTGTGCTGTGCTGCTGCTGCTG 915
 Oy 994 GCTACCAAGCGGTGAAGCCCAAGCTTACATCAATTTGGGAGTGAAGTGAAGTGAAG 1053
 Db 916 GCTACCAAGCGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 975
 Oy 1054 AAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1104
 Db 976 AAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1035

QY 1105 CCACCATCTGCTTCAAGCTCAACCCCAAGTTCCAGTCTCTCTCCATTCCTCCCTTACATCT 1164
 DB 1036 CCATCTCAGAGGCTTCAACCCCAAGCTTCAAGTCTCTCTCCATTCCTCCCTTACATCT 1095
 QY 1165 CCTGTGACCGGTTCGAATCTTGGAG-----CGTGCATCTCTCTCCAGGAGAGG 1215
 DB 1096 CCACCTCAGCTTATACCCCGGTGACTCTCCCACTTTCGGCTCTCCGAGAGAGGTGG 1155
 QY 1216 CCCCCCGCATCTTAAAGCTGAGCCCATCTCTCCGAGGAGCTCCGAGCTTCAACCACTCT 1275
 DB 1156 CACCACCTTATCAGAGGAGCTGACCCCATCT----- 1186
 QY 1276 GTACCCCGGGGCTCCGAGCTTCAACCACTCTCTGATCCCGGAGGCTTCGGGCTTCAACC 1335
 DB 1187 -----TGCAGACAGCCCTCTCCCTCCGAC 1209
 QY 1336 ACCTCTGACCCCAAGTTCAAGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1395
 DB 1210 CCATCTCCCAAGCTTCTCAAGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1266
 QY 1396 CGAGTCCGAGACCCCGGAGACCTCTGATACGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAG 1455
 DB 1267 ACACCTGATGACCCCGGAGAGCTGATACGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1326
 QY 1456 AGGAGTGTGTGGGCGGTGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1515
 DB 1327 AGGAGTGTGTGGGCGGTGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1386
 QY 1516 ACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1575
 DB 1387 ACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1446
 QY 1576 CGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1635
 DB 1447 CGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1596
 QY 1636 GTTCCCTGAGAAATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1695
 DB 1507 GTTCCCTGAGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1566
 QY 1696 GCTTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1724
 DB 1567 GTTCTCTCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1595

RESULT 6
 US-10-120-397-1
 : Sequence 1, Application US/10120397
 : Publication No. US20020142357A1
 :
 : GENERAL INFORMATION:
 : APPLICANT: WALLACH, David
 : BRAKEBUSCH, Cord
 : TITLE OF INVENTION: TNP RECEPTOR ACTION MODULATION
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEIMARK
 : STREET: 419 Seventh Street, N.W.
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/10/120.397
 : FILING DATE: 12-Apr-2002
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/08/054.970
 : FILING DATE: 03-MAY-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: WALLACH-9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 :
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2175 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 256..1620
 :
 : SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-120-397-1

Query Match 29.8%; Score 727; DB 13; Length 2175;
 Best Local Similarity 69.6%; Pred. No. 2.8e-174;
 Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

QY 148 TGTCCCGCCCGAGTCTCAACCTTCACTCCCGAGCCCGAGGAGGAGGAGGAGGAGGAGGAGG 207
 DB 110 TCTCTATGCGCGAGTCTCAACCTTCACTCTCAACCTTCAACCTTCAACCTTCAACCTTCAAC 169
 QY 208 TACGAGAGAGCCTGT 266
 DB 170 AGACCGAGTCCCGGAGAGCCCGAGCACTGCGCTGCGACACACTGCGCTGAGACCCCAATGAG 229
 QY 267 GAAATTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 326
 DB 230 GAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 288
 QY 327 CCACTGTGTCTTCAGCTGT 386
 DB 289 CCGCTGTGTCTTCAGAGCTGT 348
 QY 387 CTTCACCCCGGAGAGCTTGAAG 446
 DB 349 CTTCACCTAGGAGGAG 408
 QY 447 CCGCAAAATAGACCAATTGCTGTCACCAAGTGCACAAAGTACCTATCTGTCAATGAC 506
 DB 409 CTTCAAAATATATTCGATTGTCTTACCAAGTGCACAAAGTACCTATCTGTCAATGAC 468
 QY 507 TGTCCGGGTCAGAGGAG 566
 DB 469 TGTCCAGGCGCGGAG 528
 QY 567 TTGAGAGACATTTCAAG 626
 DB 529 TCGAAAAACCACTTCAG 588
 QY 627 GTGAGAGTTTGGCTGT 686
 DB 589 GTGAGAGTCTTCTTGT 648
 QY 687 TACCGGAAATACTGGGAGTGAATCTGCTTCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 746
 DB 649 TACCGGAAATATTGAGTGAATCTTTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 708
 QY 747 GGCAGAGTGAATATCTCCCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 806
 DB 709 GGCAGCGTGAACCTTCTCTGCGAG 768
 QY 807 TTCTTCTTAAAGGAGGAG 863
 DB 769 TTCTTCTTAAAG 828

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Oy 864 GAGAGTTATGTCCAAACCCGACTTCACTGTGTAAGACTCTCAGAGACCCAGCCACTACA 923
Db 869 ACGAAGTTGTGCTTACCCAGATTGAGATGTTAAAGGCACTGAGAGACTCAGGACCA 888
Oy 924 GTACTATTACCCCTGTGTATGTTCTTGGGCTTTGCTGCGATCTTGCTGTCTC 983
Db 889 GTGCTGTGCTTGTGATTTCTTTGATCTTTGCTTTTATCCCTCTTCAATGAT 948
Oy 984 TTAGCATGTGCTTACAGGCGTGAAGCCAGCTCTCTCATCATTTTGGGGGAGTGG 1043
Db 949 TTAATGTAATCGTACCAAGGAGGAGTCAAGCTCTCATGTTTGTGGAAATCG 1008
Oy 1044 ACTGTGTAAAGAGGGGAGCCAGAA-----CTCTGTGTCCGAGCCCAAGCTTC 1094
Db 1009 ACACGTGAAAAGAGGGGAGGTTGAAGAACTACTACTAGCCCTGAGCCCAAAACCA 1068
Oy 1095 AACCCCAACCAACCATCTGCTTCAAGTTCACCCCAAGTTCCAGTCTGTCTCCATTCC 1154
Db 1069 AGCTTCAGTCCCACTCAAGGCTTCAACCCCACTGAGCTTCAAGTCCGTCAGTTCC 1128
Oy 1155 CTTTCAATCTCTGTGACCGGTCCAACTTTCGAG-----CGTGGCATCTTCCCTCC 1205
Db 1129 ACTTTCACCTTCAAGTCCATACCTATACCCCGGTGACTGTCCCACTTTCGAGCTCCGC 1188
Oy 1206 AGCAGAGAGGCGCCGCTCCATCTAAAGGCTGAGCCCATCTCCCGGAGCTCCGCTCC 1265
Db 1189 AGAGAGGTGGCAACCCATATAGGGGGCTGACCCCATCT----- 1229
Oy 1266 ACCCACTGTGTACCCCGGGGCTCCGGCTTCACCCCACTGTATCCCGGAGCTCCG 1325
Db 1230 -----TCCGACACCCCTC 1242
Oy 1326 GCTTCACCCACCTCTGACCCCGCATTCAGAAAGTGGAAAGCCAGGCCCCAGGCCCC 1385
Db 1243 GCTTCAGACCCCATCTCCAAACCCCTTCAGAAAGTGGAAAGCCAGGCCCCA---AGCCA 1299
Oy 1386 GATCACTCGCGGATGCCGACCCCGGACCTCTGTAACGCGTGTGTGAGAGCGCTGCCCG 1445
Db 1300 CAGAGCTTAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1359
Oy 1446 TCGCGCTGGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1505
Db 1360 TTGCGCTGGAAGAAATTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1419
Oy 1506 GAGCTGGAAGAAAGCGGCGCACTGGCGGAGGCGGAGTACAGATCTGTGGCGGCTGGCGG 1565
Db 1420 GAGCTGCAAAAGCGGCGCTGCTGGCGAGGCGCAATACAGATCTGTGGCGGCTGGAGG 1479
Oy 1566 CGCGCGACGCGCGCGCGCGAGGCGACGCTGTGAGCTGTGGCGCGGCTGTCAAGGACATG 1625
Db 1480 CGGCGCAACCGCGCGCGCGCGAGGCGACGCTGTGAGCTGTGGCGCGGCTGTCCGACATG 1539
Oy 1626 GACCTGTGTGGTGTGCTGTGAAAAATAGAGAGGCGCTGTGGCGCGGCGCGCTGTGGCG 1685
Db 1540 GACCTGTGTGGCTGTGCTGTGAGAGACATGAGAGGCGCTTGTGGCGCGGCGCGCTGTGG 1599
Oy 1686 TCGGAGCGCGCGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1745
Db 1600 CGCGCGCGCGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1659
Oy 1746 C 1746
Db 1660 C 1660

```

RESULT 7
US-09-880-107-2360
Sequence 2360, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:

APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe

```

; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 2360
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M58286
US-09-880-107-2360

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Query Match 29.7%; Score 725.8; DB 10; Length 2111;
Best Local Similarity 70.0%; Pred. No. 5,66-174;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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Oy 148 TGTCCCGCCCGCACTCTCAACCTTCACTCCCGAGCCCGAGCCCGGCTTCCACTGGCA 207
Db 41 TCTATATGCCGAGTCTCAACCTTCAACCTTCACTCCCGAGCCCGAGCCCGGCTTCCACTGG 100
Oy 208 TACCGAGAGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 266
Db 101 AGACCGAGTCCCGGAGAGCCCGAGCCCGGCTTCCACTCCCGAGCCCGGCTTCCACTGG 160
Oy 267 GGATTGAGAGGCGCACAGCTGGCCGAGATGAGGCTTCCCGAGCCCGGCTTCCACTGGCTG 326
Db 161 GAGTGTGAGAGGCGCACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 219
Oy 327 CCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 386
Db 220 CCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 279
Oy 387 CCTCACCCCGGAGACCTGTGAGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 446
Db 280 CCTCACCTGTGAGAGAGAGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 339
Oy 447 CCGCAAAATAGACACATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 506
Db 340 CTTCAAAATATTTGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 399
Oy 507 TGTTCGGGTCCAGGCGAGACAGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 566
Db 400 TGTTCAGGCGCGGAGAGATACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 459
Oy 567 TTGAGAAACCTCTCAACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 626
Db 460 TCAGAAACCACTTCAACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 519
Oy 627 GTGAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 686
Db 520 GTGAGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
Oy 687 TACCGGAAATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 746
Db 580 TACCGGATTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 639
Oy 747 GGCACAGTGAATATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 806
Db 640 GGCACCGTGAACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
Oy 807 TTTCTTTCTTAAGGCGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 863
Db 700 TTTCTTTCTTAAGGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 759
Oy 864 GAGAGTTATGTCCAAACCCGACTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 923

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Db	541	TCCTGTACTAAGTGTAAAGAAAGCCCTGAGTGTACAGAAAGTTGTGCTACCCCAAGTTGAG	600
Qy	891	ACTGTAAAGACTCTCAGAGCCCAAGCACTACAGTACTATTAACCCCTGGTATTTGCTTTC	950
Db	601	AATGTAAAGGCACTGAGAGACTCAGAGCAACAGAGTGTGTGCCCCCTGGTCAATTTCTTT	660
Qy	951	GAGGCTTGTGCTGGGCAATCTGTGGCCCTGTGTGCTGTAGCATGTGCGTTACCAAGCGGTGAG	1010
Db	661	GATCTTGTGCTTTTATCCCTCTCTTCAATTGGTTTAAATGATGTGCTTACCAAGGTTGAA	720
Qy	1011	CCCAAGCTCTACTCCATCATTTTGCAGGAGCATGTGCACTGTGTAAAGAGGGAGGCCAGAA	1070
Db	721	TCGAAGCTCTACTCATTTGTTTGTGTGAAATGTGACACCGTAAAGAGAGGGAGGCTTGA	780
Qy	1071	-----CTCTGTGTCCCGGCCCCAGGCTTCAACCCCAACCAACCATCTGTCTTCAACG	1120
Db	781	GGAATCTACTACTAAGCCCCCTGGCCCCCAACCCAACTTCAAGTCCCACTCAGGCTTCAAC	840
Qy	1122	TCACCCCAAGTTCCAGTCTGTCTCCATTTCCCCCTTACATCTCTGTGAACCGTCCAA	1180
Db	841	CCCACTCCGCTGTAGTCCGTGCGTGCAGTGTCTCACTTCACTTCACTCAGCTCAACTATAC	900
Qy	1182	TTTCGAG-----CCGTGCACTCTCCCTTCAGAGAGACGAGCCCCGCCCATCTAAAG	1230
Db	901	CCCGGTGACTGTCCCAACTTTTGCGGCTCCCGCAGAGAGTGTGACACACCTATAGAGG	960
Qy	1233	GCTGAGCCCATCTCTCCGAGGCGCTTCGAGCTTCAGCCCATCTTGTATCCCGGAGGCTCG	1290
Db	961	GCTGACCCCATCTCTTGCACAGCCCTCGCGCTCCAGCCCATCC-----	1000
Qy	1293	GCCTCCACCCACTCTGTATCCCGGAGGCTCCGCGCTTCACCCCACTCTGCACCCCAATT	1350
Db	1005	-----CAACCCCTT	1010
Qy	1353	CAGAAAGTGAAGCAGAGCCCCCAAGCGCCCGATACAGCTCGCGGATGCGCAACCCCGG	1410
Db	1015	CAGAAAGTGAAGACAGGCCCCACA---AGCCACAGAGCTTATGAACTGATATACCCCGG	1070
Qy	1413	ACCCTGTACGCGGTGTGTGACAGCGCTGCCCGCGCTGAGAGAGATTGTGTGCGCG	1470
Db	1072	ACGCTGTACGCGGTGTGTGAGAACGTGCCCGCGTTCGCTGTGAAAGAAATTGCTGTGCGCG	1130
Qy	1473	CTGGGACTGAGCGAGACAGAGATCGAGGCGCTGTGAGCTGTGAGAAACGGGCGCCACTGTGCG	1530
Db	1132	CTAGGGCTGAGAGCAACAGAGATTCATCGGCTGTGAGCTGTGACAAACGGGCGCTGTGCGCG	1190
Qy	1533	GAGGCGCATGTACAGATGCTGGCGGCGCTGTGAGGCGGCGCAGCGCGCGGCGAGGCCAAG	1590
Db	1192	GAGGCGCAATACAGATGTGTGCGACCTGTGAGGCGGCGGCGCGCGCGGCGCGAGGCCAAG	1250
Qy	1593	CTGAGCTGTGTGAGCCGCGGTGTCTCAGAGACATGAGACTTGTGGTGTTCCTGTGAAACATA	1650
Db	1252	CTGAGAGCTGTGTGAGACGGGTGTCTCGCGACACATGAGACTGTGTGGCTGTGTGAGAGACATC	1310
Qy	1653	GAGGAGCGCTGTGAGGTGTGCGCGCGCGCGCTCGCGCTGTGAGACCCCGCTTCTGTGTGA	1700
Db	1312	GAGGAGCGCTTGTGTGCGCGCGCGCGCGCTCGCGCGCGCGCGCGCATCTTCTCAGATGA	1360

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PRIORITY APPLICATION NUMBER: 09/792,356
PRIORITY FILING DATE: 2000-02-23
PRIORITY APPLICATION NUMBER: 08/477,639
PRIORITY FILING DATE: 1995-06-07
PRIORITY APPLICATION NUMBER: 08/383,676
PRIORITY FILING DATE: 1995-02-01
PRIORITY APPLICATION NUMBER: 08/153,287
PRIORITY FILING DATE: 1993-11-17
PRIORITY APPLICATION NUMBER: 07/821,750
PRIORITY FILING DATE: 1992-01-02
PRIORITY APPLICATION NUMBER: 07/511,430
PRIORITY FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1368
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1365)
NAME/KEY: sig_peptide
LOCATION: (1)..(87)
NAME/KEY: misc_feature
LOCATION: (88)..(120)
OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion
NAME/KEY: misc_feature
LOCATION: (606)..(633)
OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion
US-09-899-429A-1

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Query Match	28.1%;	Score 685.4;	DB 10;	Length 1368;
Best Local Similarity	71.1%;	Pred. No. 8.9e-164;		
Matches 1021;	Conservative	0;	Mismatches 326;	Indels 90; Gaps 5

QY	294	ATGGGCGCTCCCGACCGGCGCTGGGCTGTGTCACGCGGAGCTTTCCAGCTCTGTGGGAC	353
Db	1	ATGGGCGCTCTCCACCGGCGCTGACCTGTGTGTGCACATGCGGCTCTCGAGCTGTGGTG	60
QY	354	GATGTGTATACCCCGCAGGAGGTTCAAGGAGCTGTCTCCTCAACC CGGAGACCTTGAGAGAGAGA	413
Db	61	GGAATATATACCCCTCAGGGGTTATTGGACTGTGTCTCTCACTTAAAGGAGACAGGAGAAAGAGA	120
QY	414	GAGAGTCCCTGTCCCGCAAGAAAATATTAACCAACCGCAAAATAGACACATTTGCTGCACC	473
Db	121	GATAGTGTGTGTCCCGCAAGAAAATATATCCACCCTCAAAATATATTCGATTTGTCTGCTACC	180
QY	474	AAGTGCACAAAGGTACCTATCTGTACATGACTGTCCGGGTCCAAGGCGAGACACGGAC	533
Db	181	AAGTGCACAAAGGAACTTACTTGTACATGACTGTCCAAGGCGCGGCGAGATATCGGAC	240
QY	534	TGCAGGCTGTGTGCCCCCTGTGCACCTTACATCTGCTTGGAGAACATCTCAGACGATGCTCTG	593
Db	241	TGCAGGAGGTGTGAGACGGGCTCCTTCAACGGCTTCAGAAAACCACTTCAGACATCGCTTC	300
QY	594	AGCTGCTCCAGAGTACCGGAGACGAATGTTTCCAGGTGAGATTTTGGCTTGTGTAGTGCAC	653
Db	301	AGCTGCTCCAAATCCCGAAGAGAAATGGGTCAAGTGGAGATCTCTTTCTTGCACAGTGCAC	360
QY	654	CGGACACATGTGTGCGGCTGCAAGAGAAGAACAGTACCGGGAATATCTGGGGTGAAAACTGGC	713
Db	361	CGGACACACCGTGTGTGGCTGCAAGAGAAGAACAGTACCGGCAATTATTTGAGTGAATAAACCTT	420
QY	714	TTCCGCTGTCTGAACCTGCAGCCTCTGTTCCTCAATGGCACAGTATATCCCTCTGCCAGAGAG	773
Db	421	TTCCAGTGTCTTCAATTTGCAGCCTCTGTCTCAATGGGACCGTGCACCTCTCCCTGCCAGGAG	480
QY	774	AGACAGGACACATCTGCACTGCAATATGGGCTTCTTTTAAAGGCGCAAGTCAATC	833
Db	481	AAACAGAAACACCGTGTGCACCTGCAATGCAAGTATCTTTCTTAAGGAAAACGAGTGTGTC	540


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Qy      834 TCCTGTCTGATTTGTAAGAA---CAGGAGTCCGAGAGTATATGTCAACCCGACCTTCA 890
Db      541 TCCTGTCTGATTTGTAAGAAAGCTTGAGTGCAGAGAGTGTCTTACCCGAGATTAG 600
Qy      891 ACTGTAAGAGCTCTCAGAGCCAGGACCTACAGTACTATTACCCTGATTTGTCTTC 950
Db      601 AATGTAAGGACATGAGAGACTGAGGACACAGAGTGTCTTCCCTGTATTTCTTT 660
Qy      951 GGGCTTTGCTGGGATCTTGTGCTCTGTGTCTTTAGCATGTGTACAGCGGTGAAG 1010
Db      661 GGTCTTTGCTTTTATCCCTCTCTTCAATGTGTTAATGATTCGACCAACGGGTGAAG 720
Qy      1011 CCGAAGCTCTACTCCATGATTTTGGCGGAGTGCAGTCTGTGTAAAGAGGGGAGCCAGAA 1070
Db      721 TCAGAGCTCTACTCCATGATTTTGGGAGAAATGACACCTGAAAAAGGGGAGGCTTGA 780
Qy      1071 -----CTCTGTGTCCTGGGAGCCGAGGCTTCAACCCGACACCATCTGTGAGC 1121
Db      781 GGAAGTACTAGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy      1122 TCCAGCCCAAGTTCAGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1181
Db      841 CCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy      1182 TTGGAG-----CGTGTGATCTTCCCTCCAGCGAGAGGCGCCCGCTCAATTAAG 1232
Db      901 CCGGTGTGCTGTCCCAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy      1233 GCTGCGCCCATCTCTCCGCGGCTCTCCGCTCTCCAGCCCATCTGTATCCCGGGGCTCCG 1292
Db      961 GCTACCCCATCTCTGCGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1004
Qy      1293 GCTTCCACCACTCTGTATCCCGCGGCTCTCCAGCCCATCTGTGACCCCATGTT 1352
Db      1005 -----CAACCCCTT 1014
Qy      1353 CAGAGTGGAGAGCAGCGCCCGGAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1412
Db      1015 CAGAGTGGAGAGCAGCGCCCGGAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1071
Qy      1413 ACCGTGTACGCTGTGTGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1472
Db      1072 ACGGTGTACGCTGTGTGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1131
Qy      1473 CTGGAATGAGCGACGACGAGATGAGCGGCTGAGCTGAGAAAGCGGCGGCACTTGC 1532
Db      1132 CTAGGGCTGAGCGACGACGAGATGAGCTGAGCTGAGAAAGCGGCGGCTGCTGCG 1191
Qy      1533 GAGCGGAGTACAGCATGCTGCGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1592
Db      1192 GAGCGGAGTACAGCATGCTGCGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1251
Qy      1593 CTGAGCTGTGCTGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1652
Db      1252 CTGAGCTGTGCTGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
Qy      1653 GAGAGGCGCTGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1709
Db      1312 GAGAGGCGCTGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1368

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RESULT 12

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US-10-252-408-3
; Sequence 3, Application US/10252408
; Publication No. US20030082736A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
; FILE REFERENCE: A-71592
; CURRENT APPLICATION NUMBER: US/10/252,408
; PRIORITY FILING DATE: 2002-09-24
; PRIORITY APPLICATION NUMBER: US/08/406,824
; PRIORITY FILING DATE: 1995-03-20

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; PRIOR APPLICATION NUMBER: US 08/255,849
; PRIOR FILING DATE: 1994-06-08
; PRIOR APPLICATION NUMBER: US 07/860,710
; PRIOR FILING DATE: 1992-03-30
; PRIOR APPLICATION NUMBER: US 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: US 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: US 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: US 07/403,241
; PRIOR FILING DATE: 1989-09-05
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (121)..()
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(120)
; OTHER INFORMATION:
; US-10-252-408-3

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Query Match      28.04; Score 683.8; DB 14; Length 1368;
Best Local Similarity 71.04; Pred. No 2.3e-163;
Matches 1020; Conservative 0; Mismatches 327; Indels 90; Gaps 5;

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Db      61 GGAATATACCCCGGAGGGGTTCAGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy      414 GAGATCTCCCTGTGCTCCCAAGGAAATATTAACCCCGGAAATATGACCATTTGCTGCACC 473
Db      121 GATATGTGTGTCTCCCAAGGAAATATTAACCCCGGAAATATGACCATTTGCTGCACC 180
Qy      474 AAGTGCACAAAGTACTTATCTGTACATGACTGTCCGGGTCCAGGCGAGACGAGAC 533
Db      181 AAGTGCACAAAGTACTTATCTGTACATGACTGTCCGGGTCCAGGCGAGACGAGAC 240
Qy      534 TGAAGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 593
Db      241 TGAAGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy      594 AGTGTCTCAGTGTGCGGAGCAATATGTTCCAGGTGAGATTTGGCTGTGTAGTGAAC 653
Db      301 AGTGTCTCAGTGTGCGGAGCAATATGTTCCAGGTGAGATTTGGCTGTGTAGTGAAC 360
Qy      654 CCGGACACTGTGTGCGGCTGCGAGAGAAACCACTACCGGAAATATGAGGCTGCACTGCG 713
Db      361 CCGGACACTGTGTGCGGCTGCGAGAGAAACCACTACCGGAAATATGAGGCTGCACTGCG 420
Qy      714 TTCCGATGTCTGAATGCAAGCCCTGTCCCATATGAGCAAGTGAATATCCCTTCCAGAG 773
Db      421 TTCCGATGTCTGAATGCAAGCCCTGTCCCATATGAGCAAGTGAATATCCCTTCCAGAG 480
Qy      774 AGACAGAGACCATCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 833
Db      481 AAGCAAGACCGGTGTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 540
Qy      834 TCCTGTCTGATTTGTAAGAA---CAGGAGTCCGAGAGTATATGTCAACCCGACCTTCA 890

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QY 1496 CGAGCGCTGAGCTGAGAAAGGCGCCACCTGCGCGAGGCGAGTACAGCATGCTGGC 1555
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 QY 1556 GGCCTGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1615
 DB 1184 GACCTGAGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1243
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 DB 1244 CCGGAGCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1303
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RESULT 15

US-10-157-391-18
 : Sequence 18, Application US/10157391
 : Publication No. US20030166279A1
 : GENERAL INFORMATION:
 : APPLICANT: Sabbadini, Roger A.
 : APPLICANT: Neil Berkley
 : TITLE OF INVENTION: MINICELL-BASED TRANSFECTION
 : FILE REFERENCE: MPX 008DV14
 : CURRENT APPLICATION NUMBER: US/10/157,391
 : CURRENT FILING DATE: 2002-05-28
 : PRIOR APPLICATION NUMBER: 60/293,566
 : PRIOR FILING DATE: 2001-05-24
 : PRIOR APPLICATION NUMBER: 60/359,843
 : PRIOR FILING DATE: 2002-02-25
 : PRIOR APPLICATION NUMBER: 10/154,951
 : PRIOR FILING DATE: 2002-05-24
 : NUMBER OF SEQ ID NOS: 257
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 18
 : LENGTH: 1380
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Fusion protein
 : US-10-157-391-18

Query March 25.7%: Score 628; DB 12: Length 1380;

Best Local Similarity 70.5%; Pred. No. 3,1e-14; Matches 954; Conservative 0; Mismatches 310; Indels 90; Gaps 5;

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 DB 53 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 112
 QY 437 ATATTAACACCCGCAAAATAGACCAATTTGCTGCAACAAAGTCCCAAAAGTACTATCT 496
 DB 113 ATATTAACACCCGCAAAATAGACCAATTTGCTGCAACAAAGTCCCAAAAGTACTATCT 172
 QY 497 GTACAATGATGCTGCGGCTGCAAGGCGAGACACGAGCTGCAAGGCTGCAAGGCTG 556
 DB 173 GTACAATGATGCTGCGGCTGCAAGGCGAGACACGAGCTGCAAGGCTGCAAGGCTG 232
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 DB 233 CTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 292
 QY 617 AATGCTCAGTGAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
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 QY 677 GAAGAAACAGTGAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 736
 DB 353 GAAGAAACAGTGAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 412
 QY 737 CTGTCCTCAATGAGCAAGTAAATATCCCTGCTGAGAGAGACAGACCAATCTGCACTG 796

DB 413 CTGCTCAATGAGCAAGTAAATATCCCTGCTGAGAGAGACAGACCAATCTGCACTG 472
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 DB 473 CCAATAGGCTCTTCTTAAAGGCGCAAGTGAATCTTCTGCTGATGATGTAAGAAAG 532
 QY 854 CAAGAGTGAAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913
 DB 533 CTGGAATGACAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
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 DB 593 AGGCACTACAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652
 QY 974 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1033
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 QY 1034 CCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1084
 DB 713 TGGGAAATTCAGACCTGAAAGGCGGAGCTGAAAGAACTACTAGAGCCCTGCTGCT 772
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 DB 773 CCGAAACCCCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 832
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 DB 833 GCGCAATTCAGACCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 892
 QY 1196 ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1255
 DB 893 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
 QY 1256 TCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1315
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 QY 1316 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1375
 DB 974 -----CAACCTCTTCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1006
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 DB 1064 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
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 DB 1124 CGATGCTGCTGAGAGTGAAGAAAGGCGGCTGCTGCGGAGAGCGGAGAGAGAGAGAG 1183
 QY 1556 GGCCTGCGCGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1615
 DB 1184 GACCTGAGAGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1243
 QY 1616 CAGGAGCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1675
 DB 1244 CCGGAGCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1303
 QY 1676 CCGCTGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1709
 DB 1304 CGCCTCCCG 1337

Search completed: September 15, 2003, 09:29:04
Job time : 454 sec

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QY <td>Db</td> <td>601</td> <td>TCTCAGCTGCTGAGTGTGTGTGTGTGTGT</td> <td>630</td>	Db	601	TCTCAGCTGCTGAGTGTGTGTGTGTGTGT	630
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DEFINITION		688899 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.		
ACCESSION		CB439280		
VERSION		CB439280.1		
KEYWORDS		EST.		
SOURCE		Bos taurus (cow)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.		
REFERENCE		1 (bases 1 to 632)		
AUTHORS		Smith,T.P.L., Roberts,A.U., Echterkamp,S.B., Chitko-McKown,C.G., Wray,J.E. and Keeler,J.W.		
TITLE		A second set of bovine ESTs from pooled-tissue normalized libraries		
JOURNAL		unpublished		
COMMENT		Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smitht@mail.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alc option. Vector identified with cross_match v0.990329. Plate: PCY8044 row: N column: 10 Seq primer: TAGAAGCAGCAGTCGAG. Location/Qualifiers		
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		/ligase_type="pooled"		
		/lab_host="DH10B"		
		/clone_lib="MARC 6BOV"		
		/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."		
BASE COUNT		172 a 185 c 154 g 121 t		
ORIGIN				
Query Match		25.7%; Score 627.4; DB 14; Length 632;		
Best Local Similarity		99.8%; Pred. No. 1.3e-97;		
Matches 628; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
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QY	Db	632	GTGCAGGACACCCGGAGAGATCTGCAGAGCCCTGAGACCTCTTTGTTTGT	573
QY	Db	1826	TTTTTCTGAGAGAGTCTTGAGAGAGCAGACTGTGGCAGCAGTGAAGCTGTGC	1885
QY	Db	572	TTTTTCTGAGAGAGTCTTGAGAGAGCAGACTGTGGCAGCAGTGAAGCTGTGC	513
QY	Db	1886	TACTCAGTCAATGTACATAGCTTTTCTCAGCTGCCCTGAGTGTGTGTGTGTGT	1945

Df		512	TACTCACTCAGTGAACATGTTTTCACAGTCGCCTAGAGTGTCGTGGTAGTGTG	455
Oy		1946	TGTCGTGGCGTGAAGTCCGCTGTGTGTGTCTCTCTGTATGTGCGTCTGTGTATGTGAAGTGT	2005
Df		452	TGTCGTGGCGTGAAGTCCGCTGTGTGTGTCTCTCTGTATGTGCGTCTGTGTATGTGAAGTGT	393
Oy		2006	GTCATCACTCGTAGAGAGAGGCCGAGAGTCCCGGAGACCAGAAGCATGTGTTCGGAAGATCAG	2055
Df		392	GTGTACTCTGTAGAGAGAGGCCGAGAGTCCCGGAGACCAGAAGCATGTGTTCGGAAGATCAG	333
Oy		2066	GGGGGCCCCCTGCTATTATGCTGTTTTTTTGGGCTTGAGAACTCAGCAAGGCGAATTGGGG	2125
Df		332	GGGGGCCCCCTGCTATTATGCTGTTTTTTTGGGCTTGAGAACTCAGCAAGGCGAATTGGGG	273
Oy		2126	AACCTACGTGCGTCCCTGAGCCGGTTTTCCGAGTAGATTAAGCCATCTTTGTATCCACTCTG	2185
Df		272	AACCTACGTGCGTCCCTGAGCCGGTTTTCCGAGTAGATTAAGCCATCTTTGTATCCACTCTG	213
Oy		2186	CACATCCACTCATCTCACTCTGTGTATCACTAATAATGAAAACCTTTGTGCGCTCGACACACT	2245
Df		212	CACATCCACTCATCTCACTCTGTGTATCACTAATAATGAAAACCTTTGTGCGCTCGACACACT	153
Oy		2246	GAACTGTCCCAGGACGCGGGGAGGACAAGAAAAATGGGGCTCCCAAGGAGGACTAGCTG	2305
Df		152	GAACTGTCCCAGGACGCGGGGAGGACAAGAAAAATGGGGCTCCCAAGGAGGACTAGCTG	93
Oy		2306	TTCACTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC	2365
Df		92	TTCACTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC	33
Oy		2366	ACTTCTGTAAATACATTAATAATCTTCCAA	2394
Df		32	ACTTCTGTAAATACATTAATAATCTTCCCAA	4
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LOCUS	CB169950/c			
DEFINITION	CB169950	659 bp	mRNA	linear EST 30-JAN-2003
ACCESSION	CZ1603001.005.R1	CSBQFXN21	testes	Bos taurus CBNA sequence.
VERSION	CB169950			
KEYWORDS	CB169950.1	GI:28156078		
SOURCE	EST.			
ORGANISM	Bos taurus (cow)			
REFERENCE	Bos taurus			
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
JOURNAL	Bovidae; Bovinae; Bos.			
COMMENT	1 (bases 1 to 659) Adelson, D.L. and Gill, C.A. Bovine ESTs (Adelson and Gill) Unpublished Contact: David L. Adelson Animal Breeding and Genetics Texas A&M University Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA Tel: 9798452616 Fax: 9798456970 Email: david.adelson@tamu.edu. Location/Organism 1. .659 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /issue_type="testes" /clone_lib="CSBQFXN21" /note="Organ: testes; Vector: pBluescript SK+; Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert (5'-NNN...NNNinsert) GCCAATTCAGCTCACCGCGGTGGGCGGCGCGCTCGAG. Sequence 3' of the inserts (AAGAAATTCGATTAACCTTATCATATACCGTCACTCGAG. normalized Rd 2 library, sequenced 3' with M13R primer."			
BASE COUNT		179 a	192 c	159 g 129 t

ORIGIN

Query Match 25.5%; Score 622.8; DB 14; Length 659;

Best Local Similarity 98.5%; Pred. No. 7,7e-97;
Matches 640; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

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 599 GTTCTGAGTGAAGAGTCTTGAGAGCAGCAGATCTGCGACCACTGCTGTGC 540
 1886 TACTACACAGTGTACATAGCTTTCTCAGCTGCTGAGTGTGTGTGTGTGTGTG 1945
 539 TACTACACAGTGTACATAGCTTTCTCAGCTGCTGAGTGTGTGTGTGTGTGTG 480
 1946 TGTCTGCGTGCAGTGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2005
 479 TGTCTGCGTGCAGTGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 2006 GTGTACTGCTGAGAGAGCCGAGTGTGCTCCGAGCCCAAGGCGAGTGTGCGAAGATAG 2065
 419 GTGTACTGCTGAGAGAGCCGAGTGTGCTCCGAGCCCAAGGCGAGTGTGCGAAGATAG 360
 2066 GGGGCGCCCTGCTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2125
 359 GGGGCGCCCTGCTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 2126 AACCTAGCTGCTGCTGCTGAGCGGTTTGCGAGTATAGCAATCTTTGTATCACTGTG 2185
 299 AACCTAGCTGCTGCTGAGCGGTTTGCGAGTATAGCAATCTTTGTATCACTGTG 240
 2186 CACATCTCACTCATCTCTGTATCACTATAGAACTTTGTTGCTGCTGAGCACT 2245
 239 CACATCTCACTCATCTCTGTATCACTATAGAACTTTGTTGCTGCTGAGCACT 180
 2246 GAACGTCTCCCGAGGAGCGGGGAGCAGAAATTTGGGGCTCCCAAGGAGCTAGTGTG 2305
 179 GAACGTCTCCCGAGGAGCGGGGAGCAGAAATTTGGGGCTCCCAAGGAGCTAGTGTG 120
 2306 TTCACTTCACTCATCTGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2365
 119 TTCACTTCACTCATCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 60
 2366 ACTTCTGTATATACATAAATCTTCAATTAAGCTTGCCTGTGAGGG 2415
 59 ACTTCTGTATATACATAAATCTTCAATTAAGCTTGCCTGTGAGGG 10

RESULT 5

CB455341 631 bp mRNA linear EST 26-MAR-2003

LOCUS 712479 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.

DEFINITION CB455341
ACCESSION CB455341
VERSION CB455341.1 GI:29261723KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurusREFERENCE 1 (bases 1 to 631)
Smith,T.P.L., Roberts,A.J., Echlernkamp,S.E., Chitko-Mckown,C.G.,
Wray,J.E. and Keefe,J.W.
A second set of bovine ESTs from pooled-tissue normalized librariesJOURNAL Unpublished
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_aln option. Vector identified with
 cross_match v0.990329.
 Plate: F0Y8070 row: E column: 3
 Seq primer: GTAAATACAGTCACTATAGG.
 Location/Qualifiers

FEATURES

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 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with RNA pooled from multiple tissues
 including liver, lung, hypothalamus, pituitary, and
 placenta/endometrium."

BASE COUNT 99 a 174 c 193 g 164 t 1 others

ORIGIN

Query Match 25.2%; Score 616; DB 14; Length 631;

Best Local Similarity 99.0%; Pred. No. 1.1e-95;
Matches 619; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 1704 TGTGAAGCCCGCCCTCCGACTGCGGCGCTCCCGCCCTGCAAGCGCTTCTTC 1763
 67 TGTGAAGCCCGCCCTCCGACTGCGGCGCTCCCGCCCTGCAAGCGCTTCTTC 126
 1764 CTGTGCCAGGAGCCCGGAAGATCTCGAATATGCGCTGTGTGTGTGTGTGTG 1823
 127 CTGTGCCAGGAGCCCGGAAGATCTCGAATATGCGCTGTGTGTGTGTGTGTG 186
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 187 TTTTCTCTGAGAGGAAGCTTGTGAGAGCAGCAGATCTGGCAGCACTGACTGT 246
 1884 GCTACTCACTAGTATAGATTTCTCACTGCTGCTGAGTGTGTGTGTGTGTG 1943
 247 GCTACTCACTAGTATAGATTTCTCACTGCTGCTGAGTGTGTGTGTGTGTG 306
 1944 TGTGTCTGCGTGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2003
 307 TGTGTCTGCGTGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 366
 2004 GTGTGTACTGCTGAGAGAGGCGGAGTGTGCGGAGCCCAAGGAGTGTGCGAAGT 2063
 367 GTGTGTACTGCTGAGAGAGGCGGAGTGTGCGGAGCCCAAGGAGTGTGCGAAGT 426
 2064 AGGGGCGCCCTGCTTATTTGCTTTTGTGAGAACTGAGAGGCGCACTTGG 2123
 427 AGGGGCGCCCTGCTTATTTGCTTTTGTGAGAACTGAGAGGCGCACTTGN 486
 2124 GGAACCTACGTGCGTCTGAGCGGTTTGCAGTATAGTATCTTTTATTCATTC 2183
 487 GGAACCTACGTGCGTCTGAGCGGTTTGCAGTATAGTATCTTTTATTCATTC 546
 2184 TGCAATCACTCATCTCTGTACACTATAGAACTTTTGTGCTGCTGAGCAG 2243
 547 TGCAATCACTCATCTCTGTACACTATAGAACTTTTGTGCTGCTGAGCAG 606
 2244 CTGAAGTCTCCCAAGGCGGCGG 2268
 607 CTGAAGTCTCCCAAGGCGGCGG 631

RESULT 6

CB467525 621 bp mRNA linear EST 26-MAR-2003

DEFINITION	733277 MARC_6BOV Bos taurus cDNA 5', mRNA sequence.																												
ACCESSION	CB467525																												
VERSION	CB467525.1 GI:29273910																												
KEYWORDS	EST.																												
SOURCE	Bos taurus (cow)																												
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;																												
REFERENCE	1 (bases 1 to 621) Smith,T.P., Roberts,A.J., Scherrenkamp,S.E., Chilko-McKown,C.G., Wray,J.E., Lee,Keele,J.W. A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished																												
JOURNAL	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel.: 402 762 4366 Fax: 402 762 4390 Email: smith@emall.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_all option. Vector identified with cross_match v0.990329. Plate: LMB8011 row: F column: 9 Seq primer: GTAAATGAGCTCATTAATGGC. Location/Qualifiers 1..621																												
FEATURES	<table border="1"><thead><tr><th>Source</th><th>/organism="Bos taurus"</th><th>/mol_type="mRNA"</th><th>/db_xref="taxon:9913"</th><th>/tissue_type="pooled"</th><th>/lab_host="DH10B"</th><th>/clone_id="MARC_6BOV"</th><th>/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; library made with RNA pooled from multiple tissues including liver, lung hypochoalams, pituitary, and placenta/endometrium."</th></tr></thead><tbody><tr><td>BASE COUNT</td><td>117 a</td><td>152 c</td><td>177 g</td><td>173 t</td><td colspan="3">2 others</td></tr><tr><td>ORIGIN</td><td colspan="6"></td></tr></tbody></table>						Source	/organism="Bos taurus"	/mol_type="mRNA"	/db_xref="taxon:9913"	/tissue_type="pooled"	/lab_host="DH10B"	/clone_id="MARC_6BOV"	/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; library made with RNA pooled from multiple tissues including liver, lung hypochoalams, pituitary, and placenta/endometrium."	BASE COUNT	117 a	152 c	177 g	173 t	2 others			ORIGIN						
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BASE COUNT	117 a	152 c	177 g	173 t	2 others																								
ORIGIN																													
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Matches	614; Conservative 0; Mismatches 5; Indels 0; Gaps 0;																												
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Dd	1 CCTGTGGAACCTCCCTGTTTGTGTTTTTCGAGAGAAGTGCTTGAGAGCAGC 60																												
Oy	1858 CACCATTGCGACGCCACTGACCTGGTGCTACTCACTCAGGTACATGACTTTTCTCACT 1917																												
Dd	61 CACGATCTGGGACGCACCTGACCTGGTGCTACTCACTCAGGTACATGACTTTTCTCACT 120																												
Oy	1918 GCCGAGGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGT 1977																												
Dd	121 GCCGAGGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGT 180																												
Oy	1978 GTATGTGCGTCTGT 2037																												
Dd	181 GTATGTGCGTCTGT 240																												
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Dd	241 AGCCCAAAGCAGCGGTTCGGAAGATGAGAGGGGGCCCTGCTTAATGTCCGTGTTTTTGGGC 300																												
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Dd	301 TTGAGAACCTCAGCAAGGCGACTGGGGGAACCTTAGTGTCGTGTCGAGCCGGTTTCGCG 360																												
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OY	2278	AAATGGGGCCCTCCCAAGGGAGCTAGCTGTTCACTTCAGTTCACTGCTCAGTGTGTCCG	2337
Db	481	AAATGGGGCCCTCCCAAGGGAGCTAGCTGTTCACTTCAGTTCACTGCTCAGTGTGTCCG	540
OY	2338	ACCTTTGGGACACCTGTGAATTCGAGGAGACTCTTGTAATACCTAAATCTTCATTA	2397
Db	541	ACCTTTGGGACACCTGTGAATTCGAGGAGACTCTTGTAATACCTAAATCTTCATTA	600
OY	2398	AAGCTGACCTCGAGGGA	2416
Db	601	AAGCTGACCTCGAGGGA	619
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DEFINITION	CB456735	714023	MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION	CB456735		
VERSION	CB456735.1	GI:29263117	
KEYWORDS	EST.		
SOURCE	Bos taurus (cow)		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 611) Smith,T.P.L., Roberts,A.J., Echeerikamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keeler,J.W.		
TITLE	A second set of bovine ESTs from pooled-tissue normalized libraries		
JOURNAL	Unpublished		
COMMENT	Contact: Smith TPL USA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smitht@mail.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_aln option. Vector identified with cross_match v0.990329 Plate: FQY8070 row: E column: 3 Seq primer: TAGAAGCACAGTCGACG3. Location/Qualifiers		
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	/clone_lib="MARC 6BOV"		
	/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."		
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Best Local Similarity	99.3%;	Pred. No. 1e-93;	
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Db	611	GTTTGTGTTTTTTTGGAGAGAAAGTCCTGGAGAGAGGACGACATCTGACGACGACGGA	552
OY	1878	CTGTGTCTACTACTCAGTGTATACATGATTTTCTCAGCTGCTGAGTGTGTCTGTGT	1937
Db	551	CTGTGTCTACTACTCAGTGTATACATGATTTTCTCAGCTGCTGAGTGTGTGTCTGTGT	492
OY	1938	GTAAGTGTGTCTGCGGCAAGTGGCTGTGTTGTCTCTGTATGTGCGTCTGTGTGATG	1997

D	b		491	GTAAGTGTGATCTGGTGAGTGGCGTAGGTTGGTCTCTGTATNTGGGTCTGTGTANTG	432
O	y		1998	TGGAATTGTGTACTTCCTGCTGAGAGAAGCCGAGATGTGCCCGAGACCCCAAGCATGTGGTCCG	2057
D	b		431	TGGAATTGTGTATCTGCTGAGAGAAGCCGAGATGTGCCCGAGACCCCAAGCATGTGGTCCG	372
O	y		2058	AAGATGAAAGGAGCACCCTGCCTTAATTGGCTGTTTTTGGGCTTGGAGAATCACTAGCAAAGCG	2117
D	b		371	AAGATGAAAGGAGCACCCTGCCTTAATTGGCTGTTTTTGGGCTTGGAGAATCACTAGCAAAGCG	312
O	y		2118	ACTTGGGGAACCTAAGTGTGGTCCCTGAGCCGGTTTGGCAGTATGATAGCCATCTTTGTAT	2177
D	b		311	ACTTGGGGAACCTAAGTGTGGTCCCTGAGCCGGTTTGGCAGTATGATAGCCATCTTTGTAT	252
O	y		2178	CCACTCTGCACATCCACTCATCTCCATCTCTGTACATAATGAAAACCTTTTGCCCGCTG	2237
D	b		251	CCACTCTGCACATCCACTCATCTCCATCTCTGTACATAATGAAAACCTTTTGCCCGCTG	192
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D	b		191	GACCAGCTGAACTGTCCCCAGGACGGGGGAGCACAGAAAAATATGGGCTCTCCAAAGGA	132
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D	b		131	GCTAGCTGTTCAGTTCAGTTCACTGTGCCTCAGTCCGTCCGATCTTTGGACCTCTGTAA	72
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D	b		71	TGCGAGGACTTCTGTAAATACACTAAATCTTCCAAATTAAGCTCTGCCCTGGAGGAC	12
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D	b		11	TGGCTGAAAAA 1	
R	E	S	U	L	T
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LOCUS	CB430512		612 bp	mRNA	linear EST 25-MAR-2003
DEFINITION	6064111 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.				
ACCESSION	CB430512				
VERSION	CB430512.1		GI:29206632		
KEYWORDS	EST,				
SOURCE	Bos taurus				
ORGANISM	Bos taurus (cow)				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;				
	Bovidae; Bovinae; Bos.				
	1 (bases 1 to 612)				
	Smith,T.P.L., Roberts,A.J., Reiterkamp,S.E., Chitko-McKown,C.G.,				
	Wray,J.E. and Keeler,J.W.				
	A second set of bovine ESTs from pooled-tissue normalized libraries				
	Unpublished				
TITLE	Contact: Smith TPL				
JOURNAL	USDA, ARS, US Meat Animal Research Center				
COMMENT	PO Box 166, Clay Center, NE 68933-0166, USA				
	Tel: 402 762 4366				
	Fax: 402 762 4390				
	Email: smitht@mail.marc.usda.gov				
	Single pass sequencing. Bases called with phred v0.020425.c and				
	trimmed with the aid of the trim_alo option. Vector identified with				
	closer_match v0.990329.				
	Plate: PQY8024 row: F column: 24				
	Seq primer: GTAATACGACTCACAATGAGG.				
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	/cbase_type="pooled"				
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	/clone_lib="MARC 6BOV"				
	/note="Vector: pCDNA3.1, Site 1: EcoRI, Site 2: NotI;				
	library made with RNA pooled from multiple tissues				

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Best Local Similarity	99.0%	Pred. No. 2e-93;			
Matches	606;	Conservative	0;	Mismatches	6;
				Indels	0;
				Gaps	0;
ORIGIN					
	including liver, lung, hypothalamus, pituitary, and placenta/endometrium."				
Query	1798	CCCTGTGACCTCCTGTTTGTGTTTGTGTTTGTGAGAGAGAGCTTTGAGGAGCAG	1857		
Db	1	CCCTGTGACCTCCTGTTTGTGTTTGTGTTTGTGAGAGAGAGCTTTGAGGAGCAG	60		
Query	1858	CACAGATCTGGAGCAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1917		
Db	61	CACAGATCTGGAGCAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	120		
Query	1918	GCCTGAGT	1977		
Db	121	GCCTGAGT	180		
Query	1978	GTATGTGCTGT	2037		
Db	181	GTATGTGCTGT	240		
Query	2038	AGCCCAAGGAGGAGT	2097		
Db	241	AGCCCAAGGAGGAGT	300		
Query	2098	TTGAGAACTCAGCAGGAGCAGCTTGGGGAACCTTACGTGTGTGTGTGTGTGTGTGT	2157		
Db	301	TTGAGAACTCAGCAGGAGCAGCTTGGGGAACCTTACGTGTGTGTGTGTGTGTGTGT	360		
Query	2158	TAGATTAAGCCATCTTTGTATTCACCTGTGACATTCATTCACCTGTGATACATAATAG	2217		
Db	361	TAGATTAAGCCATCTTTGTATTCACCTGTGACATTCATTCACCTGTGATACATAATAG	420		
Query	2218	AAACTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2277		
Db	421	AAACTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	480		
Query	2278	AAATGGGGGCTCCCAAGGAGAGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2337		
Db	481	AAATGGGGGCTCCCAAGGAGAGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540		
Query	2338	ACTCTTTGCGACCTGCTGGAATCGCAGGAGCTTCTGTAATACTAATAATCTTCAATTA	2397		
Db	541	ACTCTTTGCGACCTGCTGGAATCGCAGGAGCTTCTGTAATACTAATAATCTTCAATTA	600		
Query	2398	AAAGCTGTGCTCT 2409			
Db	601	AAAGCTGTGCTCT 612			
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LOCUS	CB437215	591 bp	mRNA	linear	EST 25-MAR-2003
DEFINITION	684655 MRC 6BOV Bos taurus cDNA 5', mRNA sequence.				
ACCESSION	CB437215				
VERSION	CB437215.1	GI:29220001			
KEYWORDS	EST.				
SOURCE	Bos taurus				
ORGANISM	Bos taurus (cow)				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.				
AUTHORS	Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keefe,J.W.				
TITLE	A second set of bovine ESTs from pooled-tissue normalized libraries				
JOURNAL	Unpublished				
COMMENT	Contact: Smith TPL				
	USDA, ARS, US Meat Animal Research Center				

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Db 166 AGGAGCGGGGAGACAGAAAAATGGGGCTCCAGAGGAGTACGTTCAGTTTCAGT 107
 QY 2317 TCAGTCGCTCAGTCTGTGCGAGCTCTTTGGCAGCCCTGTGAATCGAGGAGCTTCTGTAA 2376
 Db 106 TCAGTCGCTCAGTCTGTGCGAGCTCTTTGGCAGCCCTGTGAATCGAGGAGCTTCTGTAA 47
 QY 2377 TACACTAAATCTCCAAATTAAAGCTTCGCGCTGAGGAGC 2417
 Db 46 TACACTAAATCTCCAAATTAAAGCTTCGCGCTGAGGAGC 6

RESULT 11

AL559050 1042 bp mRNA linear EST 31-MAY-2003
 LOCUS AL559050 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 DEFINITION Homo sapiens CDNA clone CS0DJ010YB05 5-PRIME, mRNA sequence.

ACCESSION AL559050.2 GI:31283183
 VERSION AL559050
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1042)
 AUTHORS Li M.B., Gruber C., Jessee J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12904166.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
 was normalized. Library was constructed by life technologies, a
 division of invitrogen. This sequence belongs to sequence cluster
 6595.r For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DJ010CA03QPLcluster=6595.r. Contact :
 Peng Liang Email: fliang@life.com URL: <http://FullLength.invitrogen.com/>
 Faraday Avenue Genoscope sequence ID: CS0DJ010CA03QPL.

FEATURES

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 BASE COUNT 247 a 278 c 277 g 236 t 4 others

ORIGIN

Query Match 21.4%, Score 522; DB 9; Length 1042;
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 QY 142 GGGCTGTG--TCCCGCCCTCACTCAACCTTCACCTCCCGAGCCGAGGCGCGGCTC 198
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 QY 199 CACTGGGCAATACCGAGACCGTGTGTTGCTGTCATGTGCGGGGCGCCACTGCCCC-AGC 257
 Db 163 GTCCTGGACAGACGAGTCCCGGAGAGCCCAACACACTGCGGCTGCCAACAACCTGCGAGC 222

QY 258 CCGTATGGGGATTTGAGAGGACACAGCTGGCCGAGATGAGGCTCCCGACCTGCTGGC 317
 Db 223 CCAATATGGGGAGTGAAGAGCCATAGCTGTCTGG-CATGGGCTCTCCACCTGTGCTGAC 281
 QY 318 CTGCTGTGCGCACTGTGTCTTCAGCTCTGTGTGAGATGTATACCCCGAGGGTTTACG 377
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 Db 342 GAGCTGTCTCTCACTTGGAGAGAGAGAGATGTGTGTCTCCCAAGAAAA 401
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 Db 402 TATATCAACCTCAAAATATTCATTTGCTGTACCAAGTGCACAAAGTACTATCTG 461
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 Db 462 TACAATGACTGTCCAGGCGCGGCGAGAGTACGAGCTGCAAGGTGTGTGAGAGCGCTCC 521
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 QY 915 GGCATTAAGTACTATTAACCCCTGTGTATTTCTTGGGCTTTTGGCTGCTGCTGCC 974
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 Db 1002 GGGRAATCGACACCTGAAAGAGGGGAGCTTGA 1037

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DEFINITION CB536686
 ACCESSION CB536686.1 GI:29404642
 VERSION
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 519)
 AUTHORS Smith T.P.L., Roberts A.J., Echtenkamp S.E., Chiko-Mckown C.G.,
 Wray J.E. and Keefe J.W.
 TITLE A second set of bovine ESTs from pooled-tissue normalized libraries

JOURNAL
COMMENT Unpublished
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitth@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alc option. Vector identified with
cross match v0.990329.
Plate: LAM8024 row: B column: 16
Seq primer: TAGAAGCAGCTGAGG.
Location/Qualifiers
1. 519
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

FEATURES
Source
BASE COUNT 117 a 127 c 158 g 117 t
ORIGIN

Query Match 21.1%; Score 514.2; DB 14; Length 519;
Best Local Similarity 99.4%; Pred. No. 3.5e-78;
Matches 516; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 643 GTGATGAGACCGGAGACCTGTGTGCGGCTGACAGAGAAACAGTACCGGAAATAGTGG 702
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DB 459 GTGAATCTGGTCCGGTGTGTGATGACAGCTCTGTCCCAATGGGACAGTGAATATCC 400
QY 763 CCTCCAGAGAGACAGGACACCATCTGCGACCTGACATGAGGCTTTCTTTAAAGGCG 822
DB 399 CCTCCAGAGAGACAGGACACCATCTGCGACCTGACATGAGGCTTTCTTTAAAGGCG 340
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DB 339 CCAAGTGCATCTCTGTGATGATTTAGAAACAAGAGTGGAGAAATTATGTCACACC 280
QY 883 GACCTTCACTGTGTAAGACTCTCAGAGCCAGGACCTACAGTACTATTACCCCTGTGA 942
DB 279 GACCTTCACTGTGTAAGACTCTCAGAGCCAGGACCTACAGTACTATTACCCCTGTGA 220
QY 943 TTGTCTTCGGGCTTGGCTGCGATCCTGCGCTGTGTGCTTATGATGATGGTACACAGC 1002
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QY 1003 GGTGGAAGCCCAAGCTCTACTTCATCATTTTGCGGAGTGCATCTCTGTGTAAGAGGAGG 1062
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DB 39 CCACCCCAAGTTCAGTCTGTCTTCATTCCTCCCTTAAA 1

RESULT 13
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LOCUS CD288290
DEFINITION 3_P15.abd.F0R14.(Day_14_pregnant_ovine_endometrium) Ovis aries cDNA
/ mRNA sequence.

ACCESSION CD288290
VERSION CD288290.1 GI:31086333
KEYWORDS EST
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries

REFERENCE
AUTHORS Gray,C.A., Adelson,D.L. and Spencer,T.E.
TITLE Ovine ESTs
JOURNAL Unpublished
COMMENT Contact: Thomas E. Spencer
Center for Animal Biotechnology and Genomics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798454896
Fax: 9798622662
Email: tepencer@anac.tamu.edu.
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/sex="female"
/tissue_type="endometrium"
/dev_stage="Day 14 pregnant"
/clone_lib="POB14 (Day 14 pregnant ovine endometrium)"
/note="Organ: uterus; Vector: Triplex2; Site 1: EcoRI,
Site 2: XhoI; Non-normalized library, sequenced 5' with
Triplex2 primer (CTCCGAGATGTGACGCG). Library constructed
by Clontech with total RNA extracted using the Trizol
method and pooled from 5 females."

FEATURES
Source
BASE COUNT 109 a 165 c 167 g 104 t
ORIGIN

Query Match 21.0%; Score 513; DB 14; Length 545;
Best Local Similarity 96.3%; Pred. No. 5.4e-78;
Matches 525; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 187 AGCCCGGCGCTCCACTGCGCATACGAGACCGTGTGCTGTACTGTCCGGGCGCCG 246
DB 1 AGCCCGGCGCTCCACTGCGCATACGAGACCGTGTGCTGTACTGTCCGGGCGCCG 60
QY 247 ACTGCCCGAGCCCGATGAGGGGATTGAGGCGCACGCTGCGGAGACATGGGCGCTCCCA 306
DB 61 ACTGCCCGAGCCCGATGAGGGGATTGAGGCGCACGCTGCGGAGACATGGGCGCTCCCA 120
QY 307 CCGTGCCCTGCGCTCTGCTGCACTGTGTCTTCCAGCTCTGTGAGAGATGTATACCCG 366
DB 121 CCGTGCCCTGCGCTCTGCTGCACTGTGTCTTCCAGCTCTGTGAGAGATGTATACCCG 180
QY 367 CAGGGGTTCAAGGGGCTGTCTCTCAACCCCGGAGCTGAGAGAGAGAGTCCCTGTC 426
DB 181 CAGGGGTTCAAGGGGCTGTCTCTCAACCCCGGAGCTGAGAGAGAGAGTCCCTGTC 240
QY 427 CCCAAGGAATAATTAACACCCCGCAAAATAGCACTTTGTGACCAAGTGCCCAAG 486
DB 241 CCCAAGGAATAATTAACACCCCGCAAAATAGCACTTTGTGACCAAGTGCCCAAG 300
QY 487 GTACTTATCTGTAGATGACTGTCCGGGCTCAGGGGAGACACGAGTGCAGGGTGTGTG 546
DB 301 GTACTTATCTGTAGATGACTGTCCGGGCTCAGGGGAGACACGAGTGCAGGGTGTGTG 360
QY 547 CCCTGTGACCTTAACAGTGTCTTGGAGAACATTTGAGAGAGATGCTTGAAGTCTCAAGT 606
DB 361 CCCTGTGACCTTAACAGTGTCTTGGAGAACATTTGAGAGAGATGCTTGAAGTCTCAAGT 420
QY 607 GCGGAGCAAAATTTTCCAGGTGAGATTTTGCTTGTGTGTGTGAGACCGGAGACTGTGT 666
DB 421 GCGGAGTGAATATTTCCAGGTGAGATTTTGCTTGTGTGTGTGAGACCGGAGACTGTGT 480

OY 667 GCGGCTGAGAGAACAGTACCGGGAATACCTGGGTTGAACAGTGGCTTCCGGTCTGCA 726
 DB 461 GTGGCTGAGAGAACAGTACCGGGAATACCTGGGTTGAACAGTGGCTTCCGGTCTGCA 540
 OY 727 ACTGC 731
 DB 541 ACTGC 545
 RESULT 14
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 DEFINITION clone CS0D1008Y2P1 5-PRIME, mRNA sequence.
 ACCESSION BX377601
 VERSION BX377601.1 GI:30435085
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1096)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6595.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1008CH10P1&cluster=6595.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1008CH10P1.
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 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 258 a 303 c 284 g 248 t
 ORIGIN 3 others
 Query Match 21.0% Score 511.8; DB 13; Length 1096;
 Best Local Similarity 73.2%; Pred. No. 5,6e-78;
 Matches 708; Conservative 2; Mismatches 249; Indels 8; Gaps 4;

DB 294 GTTGTGGAAATATACCCCTTAGGGGTTATTGACTGATCCCTCCTAGGGAGACAGGA 353
 OY 407 GAAGAGAGAGATCCCTGTCTCCCAAGAAATATTAACCAACCCGCAAAATAGACCATTTG 466
 DB 354 GAAGAGAGATATGTGTGTCTCCCAAGAAATATATACCAACCCCTCAAAATATATGATTTG 413
 OY 467 CTGCACCAAGTCCCAAAAGTACTTATCTGTACATATGCTGTGCGGTCCAGGGCGAGA 526
 DB 414 CTGTACCAAGTCCCAAAAGTACTTATCTGTACATATGCTGTGCGGTCCAGGGCGAGA 473
 OY 527 CACGAGCTGACGGGTTGTGCCCCCTGAGCACTACCTGCTTGGAGAACATCTCAGAG 586
 DB 474 TACGAGCTGACGGGTTGTGCCCCCTGAGCACTACCTGCTTGGAGAACATCTCAGAG 533
 OY 587 ATGCTTGAAGTCTTCCAGGTCCGGGACGAAGTTCCTCAGGTGAGATTTGCTGTGT 646
 DB 534 CTGCTTGAAGTCTTCCAGGTCCGGGACGAAGTTCCTCAGGTGAGATTTGCTGTGT 593
 OY 647 AGTGACCTGGGACACTGTGTGCGGCTGTGAGAGAAACAGTACCGGAAATCTGGGGTGA 706
 DB 594 AGTGACCTGGGACACTGTGTGCGGCTGTGAGAGAAACAGTACCGGCAATTATGGAGTGA 653
 OY 707 AACTGCTTCCGGTGTCTGAACCTGACAGCTGTGCCAATGSCACAGTAAATTCCTCTG 766
 DB 654 AACTTCTTCCAGTGTCTGAACCTGACAGCTGTGCCAATGSCACAGTAAATTCCTCTG 713
 OY 767 CCAGAGAGACAGACACATCTGCACTGCAATATGAGCTTCTTTTAAAGCGCCGA 826
 DB 714 CCAGAGAGACAGACACATCTGCACTGCAATATGAGCTTCTTTTAAAGCGCCGA 773
 OY 827 GTGCATCTCTCTGTATGTTATAGAA---CAGAGTGGCAAGTATATGTCACCCG 883
 DB 774 GTGCTCTCTCTGTATGTTATAGAA---CAGAGTGGCAAGTATATGTCACCCG 833
 OY 884 ACCTTCACTGTGTAAGTCTGCACTGCAATATGAGCTTCTTTTAAAGCGCCGA 943
 DB 834 GATGAGAAATTTAAGGACCTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACT 893
 OY 944 TGTCTTGGGCTTGTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1003
 DB 894 TTTCTTGGGCTTGTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 953
 OY 1004 GTGAGAGCCAGCTATCTGCACTGCAATATGAGCTTCTTTTAAAGCGCCGA 1063
 DB 954 GTGAGAGCCAGCTATCTGCACTGCAATATGAGCTTCTTTTAAAGCGCCGA 1013
 OY 1064 GCCAGAA 1070
 DB 1014 GCTTGA 1020
 RESULT 15
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 LOCUS B1898540
 DEFINITION 479493 MARC 2Bov Bos taurus cDNA 5', mRNA sequence.
 ACCESSION B1898540
 VERSION B1898540.1 GI:16203989
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 502)
 AUTHORS Smith, T.P.L., Grose, W.M., Preking, B.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
 G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chikio-McKown, C.G.,
 Pertea, G., Holt, I., Karaycheva, S., Liang, F., Quackenbush, J. and
 Keefe, J.W.
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 JOURNAL Genome Res. 11 (4), 626-630 (2001)

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OM protein - protein search, using sw model

Run on: September 13, 2003, 06:55:24 ; Search time 47 Seconds

(without alignments)
1590.643 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2603	100.0	471 23	AAE25816
2	2603	100.0	471 23	ABE25816
3	1517	58.3	455 11	ABG74751
4	1517	58.3	455 11	ABG74755
5	1517	58.3	455 12	AAAR10986
6	1517	58.3	455 12	AAAR42059
7	1517	58.3	455 16	AAAR50894
8	1517	58.3	455 20	AAAR30934
9	1517	58.3	455 21	AAAR36266

10	1517	58.3	455 21	AAAR37800	Human tumour necro
11	1517	58.3	455 21	AAAR26984	Human TNFR 1. Hom
12	1517	58.3	455 21	AAAR23446	Human tumour necro
13	1517	58.3	455 21	AAAR01336	TNF-R1 death recep
14	1517	58.3	455 22	AAAR68817	Human TNFRP-aseoc1
15	1517	58.3	455 22	AAAR36697	Human tumour necro
16	1517	58.3	455 22	AAAR37677	Human 30 kDa TNF 1
17	1517	58.3	455 23	AAAR54799	Human COPD-related
18	1517	58.3	455 23	AAAR22286	TNFR1 expression m
19	1517	58.3	455 23	AAAR1649	Human tumour necro
20	1517	58.3	455 23	AAAR75064	Human tumour necro
21	1514	58.2	455 12	AAAR1082	Human 55kD TNF-bin
22	1511	58.0	455 13	AAAR20787	TNF-alpha binding
23	1508	57.9	455 11	AAAR07451	Human Tumour Necro
24	1508	57.9	455 14	AAAR42197	p55 Tumour necrosi
25	1505	57.8	455 14	AAAR51034	Mutant p55 tumour
26	1500.5	57.6	909 19	AAAR64485	Human Fas protein.
27	1496	57.5	453 22	AAAR50895	Human TNFR 1. Hom
28	1494	57.4	455 12	AAAR12550	Type I TNF recepto
29	1492	57.3	455 13	AAAR24000	TNF-alpha 55kd rec
30	1491	57.3	443 14	AAAR51033	Mutant p55 tumour
31	1486	55.9	433 14	AAAR51032	Mutant p55 tumour
32	1325.5	50.9	461 11	ABG74754	Rat TNF-R protein
33	1319.5	50.7	461 11	AAAR07450	Rat Tumour Necrosi
34	1319	50.7	454 23	AAAR22289	TNFR1 expression m
35	1178	45.3	371 11	ABG74753	Human TNF-RP prote
36	1178	45.3	371 11	AAAR07449	Tumour Necrosis fa
37	1072	41.2	181 23	AAAR25817	Bovine tumour necr
38	1072	41.2	280 22	ABAR8170	Soluble bovine tum
39	1019	39.1	280 22	ABAR6979	Tnfr1 protein. Un
40	834.5	32.1	213 24	ABAR99540	Amino acid sequenc
41	833	32.0	443 24	ABAR37098	Concatameric immu
42	832.5	32.0	211 20	AAAR89225	Tumour necrosis fa
43	832.5	32.0	311 20	AAAR89229	Tumour necrosis fa
44	832.5	32.0	366 20	AAAR89228	Tumour necrosis fa
45	832.5	32.0	337 20	AAAR89227	Tumour necrosis fa

ALIGNMENTS

RESULT 1
AAE25816
ID AAE25816 standard; Protein: 471 AA.

AC	AAE25816;	
XX		
XX	15-NOV-2002 (first entry)	
DT		
XX		
DE	Bovine tumour necrosis factor receptor-I (TNF-R1).	
XX		
KM	Bovine, cattle; coliform masticis; inflammatory disease; receptor;	
KM	tumour necrosis factor receptor-I; TNF-R1; antiinflammatory.	
XX		
OS	Bos taurus.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..29
FT	Protein	/label= Signal_peptide
FT		30..471
FT	Domain	/note= "Mature bovine TNF-R1"
FT		30..210
FT	Modified-site	/note= "Extracellular domain"
FT		54..56
FT	Modified-site	/note= "N-linked glycosylation site"
FT		145..147
FT	Modified-site	/note= "N-linked glycosylation site"
FT		151..153
FT	Lambda derived TNF	/note= "N-linked glycosylation site"
FT	Domain	211..235
FT		/note= "Transmembrane domain"
XX		
PN	US6406907-B1.	

XX 18-JUN-2002.
 PD 25-FEB-2000; 2000US-0513007.
 XX 26-FEB-1999; 99US-122156P.
 XX (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX (USDA) US SEC OF AGRIC.
 PA Taylor MJ, Kehrli ME, Lee E;
 XX MPI; 2002-588816/63.
 XX N-PSDB; AAD42477.
 XX Novel nucleic acid molecule encoding bovine tumor necrosis factor
 PT receptor-1 which is a potent inhibitor of tumor necrosis factor-alpha
 PT useful for treating coliform mastitis or other inflammatory disease in
 XX cattle
 XX
 PS Claim 8; Column 17-20; 16pp; English.
 CC The invention relates to an isolated nucleic acid encoding a polypeptide
 CC that binds bovine tumor necrosis factor (TNF). The invention is useful
 CC for expressing bovine TNF-R1 or soluble bovine TNF-R1 which is useful as
 CC an inhibitor of TNF in cattle suffering from coliform mastitis or other
 CC inflammatory disease. The nucleic acids and polypeptide or their
 CC fragments are useful for treating mastitis. The present sequence is
 CC bovine tumor necrosis factor receptor-1 (TNF-R1).
 CC
 XX Sequence 471 AA;
 SQ
 Query Match 100.0%; Score 2603; DB 23; Length 471;
 Best Local Similarity 100.0%; Pred. No. 8.9e-170; Mismatches 0; Indels 0; Gaps 0;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKESPCPOGKYNHPONSTICT 60
 QY 61 KCHKGTLYLNDPCPGRDTCRCVCAAGTYTALLENHRLRCLSCSRDEMFVEISPCVVD 120
 DB 61 KCHKGTLYLNDPCPGRDTCRCVCAAGTYTALLENHRLRCLSCSRDEMFVEISPCVVD 120
 QY 121 RDTVCGCRKNQRYREYWGEGFRCLNCSLCPNGTVNI PCOERODTICHMGFFLKAKCI 180
 DB 121 RDTVCGCRKNQRYREYWGEGFRCLNCSLCPNGTVNI PCOERODTICHMGFFLKAKCI 180
 QY 181 SCHDCKNKECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASPASVVLACRYORWKP 240
 DB 181 SCHDCKNKECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASPASVVLACRYORWKP 240
 QY 241 KLYSIIICGOSTLVKEGEBELLVPAPGFNPPTTICSSSPSSPVSIPIPTISCDRSNFGAV 300
 DB 241 KLYSIIICGOSTLVKEGEBELLVPAPGFNPPTTICSSSPSSPVSIPIPTISCDRSNFGAV 300
 QY 301 ASPSSETAPPHLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQKWEASA 360
 DB 301 ASPSSETAPPHLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQKWEASA 360
 QY 361 PSAPPOLADADPATYAVVDGVPSPRWKELVRLGLSEHEIRLELNGRHLREAOYSML 420
 DB 361 PSAPPOLADADPATYAVVDGVPSPRWKELVRLGLSEHEIRLELNGRHLREAOYSML 420
 QY 421 AAMRRRTPRREATLELGRVLRMDMLGLENIEEALGGAALASEPRLTW 471
 DB 421 AAMRRRTPRREATLELGRVLRMDMLGLENIEEALGGAALASEPRLTW 471
 RESULT 2
 ID ABB98169
 XX ABB98169 standard; Protein; 471 AA.

AC ABB98169;
 XX 05-NOV-2002 (first entry)
 DT Bovine tumour necrosis factor receptor-1.
 XX Bovine tumour necrosis factor receptor-1.
 DE Bovine; tumour necrosis factor receptor-1; TNF-R1; antiinflammatory;
 KW TNF cytotoxicity; mastitis; tumour necrosis factor-alpha; TNF-alpha;
 KM monoclonal antibody BC9; TNF-beta.
 XX Bos taurus.
 XX US2002076765-A1.
 XX 20-JUN-2002.
 XX 03-OCT-2001; 2001US-0970532.
 XX 26-FEB-1999; 99US-122156P.
 XX 25-FEB-2000; 2000US-0513007.
 XX (IOWA) UNIV IOWA STATE RES FOUND INC.
 PA Taylor MJ, Kehrli ME, Lee E, Mwangi S;
 XX MPI; 2002-557247/59.
 XX N-PSDB; ABQ79378.
 XX New isolated, soluble, bovine tumour necrosis factor receptor 1, useful
 PT for inhibiting tumour necrosis factor cytotoxicity for treating
 PT mastitis, is a better inhibitor of tumour necrosis factor compared to
 PT monoclonal antibody BC9 -
 XX
 PS Claim 8; Fig 1; 17pp; English.
 CC The invention relates to an isolated nucleic acid encoding bovine tumour
 CC necrosis factor receptor-1 (TNF-R1). The activity of polynucleotides of
 CC the invention may be described as antiinflammatory. Polypeptides of the
 CC invention are useful for inhibiting TNF cytotoxicity in a bovine. This is
 CC useful for treating mastitis and other inflammatory disease. Soluble
 CC bovine TNF-R1 is a better inhibitor of bovine TNF-alpha than monoclonal
 CC antibody BC9 (an antibody directed towards TNF-alpha), and can bind both
 CC TNF-alpha and TNF-beta. The current sequence represents bovine tumour
 CC necrosis factor receptor-1.
 CC
 XX Sequence 471 AA;
 SQ
 Query Match 100.0%; Score 2603; DB 23; Length 471;
 Best Local Similarity 100.0%; Pred. No. 8.9e-170; Mismatches 0; Indels 0; Gaps 0;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKESPCPOGKYNHPONSTICT 60
 DB 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKESPCPOGKYNHPONSTICT 60
 QY 61 KCHKGTLYLNDPCPGRDTCRCVCAAGTYTALLENHRLRCLSCSRDEMFVEISPCVVD 120
 DB 61 KCHKGTLYLNDPCPGRDTCRCVCAAGTYTALLENHRLRCLSCSRDEMFVEISPCVVD 120
 QY 121 RDTVCGCRKNQRYREYWGEGFRCLNCSLCPNGTVNI PCOERODTICHMGFFLKAKCI 180
 DB 121 RDTVCGCRKNQRYREYWGEGFRCLNCSLCPNGTVNI PCOERODTICHMGFFLKAKCI 180
 QY 181 SCHDCKNKECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASPASVVLACRYORWKP 240
 DB 181 SCHDCKNKECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASPASVVLACRYORWKP 240
 QY 241 KLYSIIICGOSTLVKEGEBELLVPAPGFNPPTTICSSSPSSPVSIPIPTISCDRSNFGAV 300
 DB 241 KLYSIIICGOSTLVKEGEBELLVPAPGFNPPTTICSSSPSSPVSIPIPTISCDRSNFGAV 300
 QY 301 ASPSSETAPPHLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQKWEASA 360
 DB 301 ASPSSETAPPHLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQKWEASA 360

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Db      301 ASPSETPAPHLKAGPILGPPASTHLCTGPPASTHLCTGPPASTHLCTPVQKWEASA 360
Qy      361 PSADPOLADADPATLVAVDGVPPSRWKEIVRLGLSHEIERLENGRLREAOYSML 420
Db      361 PSADPOLADADPATLVAVDGVPPSRWKEIVRLGLSHEIERLENGRLREAOYSML 420
Qy      421 AAMRRRTFRREATLELGRVLRDMDLGCLLENIEBALGGAARLASERPILW 471
Db      421 AAMRRRTFRREATLELGRVLRDMDLGCLLENIEBALGGAARLASERPILW 471

RESULT 3
ABG74751
ID      ABG74751 standard; Protein; 455 AA.
AC      ABG74751;
DT      14-MAY-2003 (first entry)
DE      Human TNF receptor protein.
XX      TNF; human; tumour necrosis factor; tumour necrosis factor receptor;
XX      TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.
XX      Homo sapiens.
XX      EP393438-A.
XX      PD      24-OCT-1990.
XX      PF      06-APR-1990; 90BP-0106624.
XX      PR      21-APR-1989; 89DE-3913101.
XX      PR      21-JUN-1989; 89DE-3920282.
XX      PA      (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX      PA      (SYND ) SYNERGEN INC.
XX      PI      Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
XX      WPI; 1990-321987/43.
XX      DR      DNA encoding TNF binding protein and TNF-receptor - used in tumour
XX      PT      treatment and to understand mechanisms to TNF action
XX      PS      Claim 22; Page 34; 51pp; German.
XX      CC      This invention describes novel polynucleotide sequences encoding tumour
XX      CC      necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).
XX      CC      The products of the invention are useful in pharmaceutical compositions
XX      CC      for prophylaxis or treatment of human tumours and to understand the
XX      CC      mechanisms of TNF action. This sequence represents the TNF receptor
XX      CC      described in the disclosure of the invention.
XX      SQ      Sequence 455 AA;

Query Match      58.3%; Score 1517; DB 11; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.4e-95;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy      1 MGLPTVPGILLPLVLPALLADYYPAGVQGLVPHPGDLKRESPCKGKYNHPONSTICT 60
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Qy      61 KCHKGTLYLNDGPGRDTDCRVACGYTALLENHRLCLSCGRCHDEMFOVEISFCVVD 120
Db      61 KCHKGTLYLNDGPGQDDTDCRECSGSPASENHLRHCLSCCKKMGQVEISSCTVD 120
Qy      121 RDTVCCGRKQVREYGETGFRLCNSLCPNGTVNIPCOERODTICHCHMGFLKAKCI 180
Db      121 RDTVCCGRKQVREYGETGFRLCNSLCPNGTVNIPCOERODTICHCHMGFLKAKCI 180
Qy      181 SCHDCRNR-ECEKLCPTPSTGKDSODPGTTVLLPLVIVGLCLASFAVYLACRYQRNK 239

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Db      181 SCGNCKSLCTKLCLEQIENVNXTEDSGTTVLLPLVIFGLCLSLFLGLWYRQRMK 240
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Qy      291 SCDSRNFCAVASPSSESTAPPHLXAGPILGPPASTHLCTGPPASTHLCTGPPASTHL 350
Db      301 PGDCPNF---AAPREVAAPPYOGADPIL-----ATL-----ASDPPI 335
Qy      351 TPVQKWEASAPADPOLADADPATLVAVDGVPPSRWKEIVRLGLSHEIERLENGR 410
Db      336 NPLQKWEDESA-HKQSLDTDDPATLVAVENVPPLRWKEIVRLGLSDHEIDRLQNGR 394
Qy      411 HLREAOYSMLAAMRRRTFRREATLELGRVLRDMDLGCLLENIEBALGGAARLASERPIL 470
Db      395 CLREAOYSMLAAMRRRTFRREATLELGRVLRDMDLGCLLENIEBALGGAARLASERPIL 454

RESULT 4
ABG74755
ID      ABG74755 standard; Protein; 455 AA.
AC      ABG74755;
DT      14-MAY-2003 (first entry)
DE      Human TNF-R protein huTNF-R.
XX      TNF; human; tumour necrosis factor; tumour necrosis factor receptor;
XX      TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.
XX      Homo sapiens.
XX      EP393438-A.
XX      PD      24-OCT-1990.
XX      PF      06-APR-1990; 90EP-0106624.
XX      PR      21-APR-1989; 89DE-3913101.
XX      PR      21-JUN-1989; 89DE-3920282.
XX      PA      (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX      PA      (SYND ) SYNERGEN INC.
XX      PI      Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
XX      WPI; 1990-321987/43.
XX      DR      N-PSDB; AB077487.
XX      PT      DNA encoding TNF binding protein and TNF-receptor - used in tumour
XX      PT      treatment and to understand mechanisms to TNF action
XX      PS      Example 9; Fig 9; 51pp; German.
XX      CC      This invention describes novel polynucleotide sequences encoding tumour
XX      CC      necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).
XX      CC      The products of the invention are useful in pharmaceutical compositions
XX      CC      for prophylaxis or treatment of human tumours and to understand the
XX      CC      mechanisms of TNF action. This sequence represents the huma TNF-R,
XX      CC      huTNF-R described in the disclosure of the invention.
XX      SQ      Sequence 455 AA;

Query Match      58.3%; Score 1517; DB 11; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.4e-95;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy      1 MGLPTVPGILLPLVLPALLADYYPAGVQGLVPHPGDLKRESPCKGKYNHPONSTICT 60
Db      1 MGLSTVPDLLPLVLLELVGLVGPVGLVPHLGDREKDSVCPOGKTIHPONNSICT 60

```


QY 61 KCHKGTLYNDGPGRPDTCRCVCAEPTTALLENHRLCLSCRCRCDENFQVEISPCVVD 120
 DB 61 KCHKGTLYNDGPGRPDTCRCVCAEPTTALLENHRLCLSCRCRCDENFQVEISPCVVD 120
 QY 121 RDTVCGCRKQRYREYWGTFRCCLNCSLCNGTNTVPCOERODTICHCHMGFPLKAKCI 180
 DB 121 RDTVCGCRKQRYREYWGTFRCCLNCSLCNGTNTVPCOERODTICHCHMGFPLKAKCI 180
 QY 181 SCHDCRKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLASFAVVLACRYQWK 239
 DB 181 SCHDCRKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLASFAVVLACRYQWK 239
 QY 240 PKYXIIICGGSTLVKEGPE-----LVPAEGFP-----TTTCGSPSTSSSPVSIIPPYI 290
 DB 240 PKYXIIICGGSTLVKEGPE-----LVPAEGFP-----TTTCGSPSTSSSPVSIIPPYI 290
 QY 291 SCDSNFGAVASPSSETAPRHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 DB 291 SCDSNFGAVASPSSETAPRHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 QY 301 PGDCPNF---AARREVAAPPYOGADPIL-----ATML-----ASDPIP 335
 DB 301 PGDCPNF---AARREVAAPPYOGADPIL-----ATML-----ASDPIP 335
 QY 351 TPVQKMEASAPSPDOLADADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGR 410
 DB 351 TPVQKMEASAPSPDOLADADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGR 410
 QY 336 NPLQKMEASA-HKPSGLDTPDPAFLYAVVENVPFLRWKGFVRGLSDHEIDRLLEONGR 394
 DB 336 NPLQKMEASA-HKPSGLDTPDPAFLYAVVENVPFLRWKGFVRGLSDHEIDRLLEONGR 394
 QY 411 HLEAQSMLAAMRRRTPRREATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPL 470
 DB 411 HLEAQSMLAAMRRRTPRREATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPL 470
 QY 395 CLREAOYSMLATWRRTPRREATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPL 454
 DB 395 CLREAOYSMLATWRRTPRREATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPL 454

RESULT 5

AAR10986
 ID AAR10986 standard; Protein; 455 AA.

XX AAR10986;

XX 25-MAR-2003 (updated)
 DT 13-MAY-1991 (first entry)

XX 30KD TNF inhibitor precursor.

XX Tumour necrosis factor; inhibitor.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Cleavage-site 40..41
 FT note="cleavage gives active protein"

XX AU9058976-A.

XX 24-JAN-1991.

XX 16-JUL-1990; 90AU-0056976.

XX 07-FEB-1990; 90US-0479661.

XX 18-JUL-1989; 89US-0381080.

XX 11-DEC-1989; 89US-0450329.

XX (SYND) SYNERGEN INC.

XX WPI; 1991-073847/11.

XX N-PSDB; AAQ10883.

XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha

XX and -beta, useful as therapeutic agent.

XX Disclousure; Fig 21; 142pp; English.

XX The sequence comprises the entire 30 kD TNF inhibitor. The clone

XX from which the sequence was deduced was isolated from a cDNA

XX library prep'd. from RNA form U937 cells treated with PMA/PHA.

CC of TNF inhibitor for use in the treatment of inflammatory and
 CC degenerative diseases. The active protein is claimed (Claim 8).
 CC See also AAR10984 and AAR11001.
 CC (updated on 25-MAR-2003 to correct PA field.)

XX Sequence 455 AA:

Query Match 58.3%; Score 1517; DB 12; Length 455;
 Best Local Similarity 62.9%; Pred. No. 1.4e-95;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLTPVPGILLPLVLPALLADVPYGVGVLPHRPEDEKRESPTQGYKNPONSITCT 60
 DB 1 MGLTPVPGILLPLVLPALLADVPYGVGVLPHRPEDEKRESPTQGYKNPONSITCT 60
 QY 61 KCHKGTLYNDGPGRPDTCRCVCAEPTTALLENHRLCLSCRCRCDENFQVEISPCVVD 120
 DB 61 KCHKGTLYNDGPGRPDTCRCVCAEPTTALLENHRLCLSCRCRCDENFQVEISPCVVD 120
 QY 121 RDTVCGCRKQRYREYWGTFRCCLNCSLCNGTNTVPCOERODTICHCHMGFPLKAKCI 180
 DB 121 RDTVCGCRKQRYREYWGTFRCCLNCSLCNGTNTVPCOERODTICHCHMGFPLKAKCI 180
 QY 181 SCHDCRKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLASFAVVLACRYQWK 239
 DB 181 SCHDCRKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLASFAVVLACRYQWK 239
 QY 240 PKYXIIICGGSTLVKEGPE-----LVPAEGFP-----TTTCGSPSTSSSPVSIIPPYI 290
 DB 240 PKYXIIICGGSTLVKEGPE-----LVPAEGFP-----TTTCGSPSTSSSPVSIIPPYI 290
 QY 291 SCDSNFGAVASPSSETAPRHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 DB 291 SCDSNFGAVASPSSETAPRHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 QY 301 PGDCPNF---AARREVAAPPYOGADPIL-----ATML-----ASDPIP 335
 DB 301 PGDCPNF---AARREVAAPPYOGADPIL-----ATML-----ASDPIP 335
 QY 351 TPVQKMEASAPSPDOLADADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGR 410
 DB 351 TPVQKMEASAPSPDOLADADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGR 410
 QY 336 NPLQKMEASA-HKPSGLDTPDPAFLYAVVENVPFLRWKGFVRGLSDHEIDRLLEONGR 394
 DB 336 NPLQKMEASA-HKPSGLDTPDPAFLYAVVENVPFLRWKGFVRGLSDHEIDRLLEONGR 394
 QY 411 HLEAQSMLAAMRRRTPRREATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPL 470
 DB 411 HLEAQSMLAAMRRRTPRREATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPL 470
 QY 395 CLREAOYSMLATWRRTPRREATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPL 454
 DB 395 CLREAOYSMLATWRRTPRREATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPL 454

RESULT 6

AAR42059
 ID AAR42059 standard; Protein; 455 AA.

XX AAR42059;

XX 25-MAR-2003 (updated)

DT 29-APR-1994 (first entry)

XX Lambda derived TNF-R.

XX Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;

XX IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;

XX rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;

XX pulmonary fibrosis; sickle cell; allograft; xenograft; rejection;

XX graft versus host disease; sepsis; inflammation; allergy;

XX autoimmune dysfunction.

XX Homo sapiens.

XX Lambda-gt10-7ctnfbp.

XX Key Location/Qualifiers

XX Peptide 1..40
 FT /note="Signal peptide"
 FT Protein 41..455
 FT /note="Mature hTNF-R"

XX W09319777-A1.

PD 14-OCT-1993.
 XX 26-MAR-1993; 93WO-US02938.
 XX 30-MAR-1992; 92US-0860710.
 XX (IMMV) IMMUNEX CORP.
 XX Smith CA;
 PI WPI, 1993-336592/42.
 DR N-PSDB; AAQ49932.
 XX New fusion protein tumour necrosis factor and human interleukin-1
 PT receptor - useful in therapy, diagnosis and assays of e.g.
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
 XX Disclosure; Page 57-59; 85pp; English.
 XX The sequences given in AAR42058-59 represent human tumour necrosis
 CC factor receptor (TNF-R) and the sequences in AAR42060-61 represent
 CC human interleukin-1 receptor (IL-1R). These sequences were used in
 CC the production of a fusion protein which conformed to one of the
 CC formulae:
 CC TNF-R-linker-TNF-R-linker-IL-1R
 CC IL-1R-linker-TNF-R-linker-TNF-R or
 CC TNF-R-linker-TNF-R-linker-TNF-R
 CC The linker may comprise 5-100 amino acids selected from Gly, Asp,
 CC Ser, Thr and Ala. These linkers separate the individual motifs
 CC by such a distance that each component of the fusion protein is
 CC capable of folding into the secondary or tertiary structure required
 CC for its biological activity. These fusion proteins may be used in
 CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
 CC particularly in conditions in which both TNF and IL-1 play a causative
 CC role. They may be used to treat cachexia, rheumatoid arthritis,
 CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
 CC cerebral malaria, allograft and xenograft rejection in graft versus
 CC host disease, sepsis, septic shock, inflammation, allergies and
 CC autoimmune dysfunctions.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 455 AA;
 SO Query Match 58.3%; Score 1517; DB 14; Length 455;
 Best Local Similarity 62.9%; Pred. NO.1.4e-95;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGLLPLVLPALLADYVPAVGGLVPHPGDLKRESPPQGRKTHPQNSTICT 60
 DB 1 MGLSTVPLLLPLVLLVGLVPGVIGLVPHLDREKRDSPVCPQGXVHPQNNISICT 60
 QY KCHGKTVYNNCPGPGRTDRCVCAPTVTALNENLRCLSSRRDMPQVETSFCVVD 120
 DB KCHGKTVYNNCPGPGRTDRCVCAPTVTALNENLRCLSSRRDMPQVETSFCVVD 120
 QY 61 KCHGKTVYNNCPGPGRTDRCVCAPTVTALNENLRCLSSRRDMPQVETSFCVVD 120
 DB 61 KCHGKTVYNNCPGPGRTDRCVCAPTVTALNENLRCLSSRRDMPQVETSFCVVD 120
 QY 121 RDTVCGCKNOYREWGRTGFCNLCSLCPNGTVNIPOEROPTCHCHMGFFLGAKCI 180
 DB 121 RDTVCGCKNOYREWGRTGFCNLCSLCPNGTVNIPOEROPTCHCHMGFFLGAKCI 180
 QY 121 RDTVCGCKNOYRHWSNENLFCGFCNCSLCNCTVHLSQDEKNYCTCHAGFFLRNKC 180
 DB 121 RDTVCGCKNOYRHWSNENLFCGFCNCSLCNCTVHLSQDEKNYCTCHAGFFLRNKC 180
 QY 181 SCHDCRKN-ECEKLCPTRPSTGKSDQDPRTVLPVIVFGLCLASPAVSLACRYQK 239
 DB 181 SCHDCRKN-ECEKLCPTRPSTGKSDQDPRTVLPVIVFGLCLASPAVSLACRYQK 239
 QY 181 SCNNCKKSLKCTKCLPQIENVKGTEDSGTVALVIFGICLISLIFIGIMRYQK 240
 DB 181 SCNNCKKSLKCTKCLPQIENVKGTEDSGTVALVIFGICLISLIFIGIMRYQK 240
 QY 240 PKLVSIIIGGOSTLVKESPE-----LVPAQGFNP-----TTTICSPSSSPVSIPI 290
 DB 240 PKLVSIIIGGOSTLVKESPE-----LVPAQGFNP-----TTTICSPSSSPVSIPI 290
 QY 291 SCDRSNFGAVASPSSETAPPHKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHL 350
 DB 291 SCDRSNFGAVASPSSETAPPHKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHL 350
 QY 301 PGDCGNF---AAPREVAAPVYGADPIL-----ATL-----ASDPIP 335
 DB 301 PGDCGNF---AAPREVAAPVYGADPIL-----ATL-----ASDPIP 335
 QY 351 TPVQWKEASAPAPQDLADADPATLYAVVDGVPSPKWEKLVRLGLSHEIRLLENGR 410
 DB 351 TPVQWKEASAPAPQDLADADPATLYAVVDGVPSPKWEKLVRLGLSHEIRLLENGR 410

DB 336 NPLQKWEOSA-HKFSQSLDTPDPAITVAIVENVPPLRNKEFVRRLGSDHEIDRLLENGR 394
 QY 411 HLREAOYSMLAARRRTPREATLELLGRVLRDMDLGCTENIEAALGAARLASEPRL 470
 DB 395 CLREAOYSMLATRRRTPREATLELLGRVLRDMDLGCTEDIEFALCGRAALPAPSLL 454

RESULT 7
 ID AAR75084
 XX AAR75084 standard; Protein; 455 AA.
 AC AAR75084;
 XX 19-JAN-1996 (first entry)
 DT p55 TNF-R.
 XX p55 TNF-R.
 XX p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
 KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
 KW phorbol myristate acetate; PMA.
 XX Homo sapiens.
 XX Location/Qualifiers
 FH Peptide
 FT 41..53
 FT /note= "N terminus of soluble p55 TNF-R"
 FT 54..56
 FT /note= "glycosylation site"
 FT Modified-site
 FT 145..147
 FT /note= "glycosylation site"
 FT Modified-site
 FT 161..163
 FT /note= "glycosylation site"
 FT Peptide
 FT 193..210
 FT /note= "peptide used in creation of chimeras"
 FT Region
 FT 198..210
 FT /note= "spacer region"
 FT Misc-difference
 FT 201
 FT /note= "major C terminus for soluble p55 TNF-R"
 FT Misc-difference
 FT 202
 FT /note= "essential for shedding reaction"
 FT Misc-difference
 FT 203
 FT /note= "minor C terminus for soluble p55 TNF-R"
 FT Region
 FT 212..234
 FT /note= "transmembrane region"
 PN AU9475742-A.
 XX 04-MAY-1995.
 PD 11-OCT-1994; 94AU-0075742;
 PF 12-OCT-1993; 93IL-0107268.
 PR (YEDA) YEDA RES & DEV CO LTD.
 PA Backin M, Brakebusch C, Varfolomeev E, Wallach D;
 PI WPI, 1995-194342/26.
 DR N-PSDB; AAQ90513.
 XX New protease capable of cleaving soluble tumour necrosis factor
 PT (TNF) receptor - from cell-bound TNF- receptor, useful for
 PT antagonising deleterious effects of TNF.
 XX Disclosure; Fig 1; 40pp; English.
 XX This sequence represents human p55 tumour necrosis factor (TNF-R).
 CC Expression of this receptor is regulated by shedding of the
 CC extracellular receptor fragment. The p55 TNF-R can be shed in response
 CC to different inducing agents, e.g. phorbol myristate acetate (PMA),
 CC depending on cell type. The only region of the receptor whose structure
 CC affects the shedding response is the spacer region (see AAR75012) in the
 CC extracellular domain. This region is located close to a site of cleavage

of the molecule, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimera between human p55 TNF-R and murine epidermal growth factor receptor (EGF-R) that are represented by AAR75007-11. This spacer region was subjected to deletion mutations (AAR75013-25) and substitutions (AAR75026-47). Of the spacer region, the most important residues are Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most important of these. The shedding of the receptor is independent of the side chain identity of these residues, with the exception of a limited dependence on the identity of Val 173. Mutations which alter the conformation of the protein adversely effect the shedding process. The mutations shown in AAR75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TNF-R from the cell bound TNF-R. Fragments of these inhibitors can be seen in AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease inhibitors can be used for enhancing TNF function.

Sequence 455 AA:

Query Match 58.3%; Score 1517; DB 16; Length 455;

Best Local Similarity 62.9%; Pred. No. 1.4e-95;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPGKRYNHPONSTICT 60
DB 1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLGDREKRSVCPGKRYIHPONNISICT 60
QY 61 KCHKGTYLYNDGPGPGDTRDCRVACPGTYTALLENHRLCLSCSRDEMFQVEISPCVVD 120
DB 61 KCHKGTYLYNDGPGPGDTRDCRVACPGTYTALLENHRLCLSCSRDEMFQVEISPCVVD 120
QY 121 RDTVCGCRKNQRYRYWGETGFRCLNCSLCPNGTVNIPCOERODTICCHMGFFLKAKCI 180
DB 121 RDTVCGCRKNQRYRYWSENLFCFCNCSLCNLTNHLSCOEKONTVCTCHAGFFLENECV 180
QY 181 SCHDCKNK-ECEKLCPTRPSTGKSDPGTTLVPLVIVFGICLASPASVVIACRYGRWK 239
DB 181 SCNNCKSKSECTKCLCPQIENYKGTEDSGTTLVPLVIFFGICLTLPLFTIGMRYGRWK 240
QY 240 PLVYSIIGCGSTLVKGEPE-----LVVAPGPNP-----TTTICSPSSPSSPVISPIPI 290
DB 241 SKLVSVICCKSTPEKEGLEGTTTYPRLADNPFSSTPGCTPLGSPVSSSTFTSSSTYT 300
QY 291 SCDSRNFCAVASPSSETAPRLKAGPILEGPPASTHLCTPGPASTHLCTPGPASTHLCT 350
DB 301 PGDCBNP---AAPREVAAPVCGADPIL-----ATAL-----ASDPIP 335
QY 351 TPVQWMSAPSAPOADADPATIYAVVDGVPSPKWEIVRRLGLSEHEIRLENGR 410
DB 336 NPLQWMSDA-HKPSGLDTPATYAVVENVPPLRWKEFVRLGISDHEIRLELONGR 394
QY 411 HLREAQYSLAMARRRTPREATLELGLRVLADMDLGLCLENIEEALGGAARLASERPL 470
DB 395 CLREAQYSLAMARRRTPREATLELGLRVLADMDLGLCLENIEEALGGAARLASERPL 454

RESULT 8

AAV30934

ID AAV30934 standard; Protein: 455 AA.

XX AAV30934;

XX 20-MAR-2003 (updated)
DT 18-OCT-1999 (first entry)

XX Human tumour necrosis factor binding protein.

XX Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
XX anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
XX autoimmune glomerulonephritis; cerebral malaria; immune response;
XX antagonist; diagnosis.

Q5 Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..29
FT /label= signal_peptide
FT Protein 30..455
FT Modified-site 34
FT /note= "hypothetical glycosylation site"
FT Modified-site 125
FT /note= "hypothetical glycosylation site"
FT Modified-site 131
FT /note= "hypothetical glycosylation site"
FT Region 212..230
FT /note= "transmembrane region"
FT Modified-site 250
FT /note= "hypothetical glycosylation site"
PN EP939121-A2.
PD 01-SEP-1999.
PP 31-AUG-1990; 99EP-0100703.
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
PR 20-APR-1990; 90CH-0001347.
PR 31-AUG-1990; 90EP-0116707.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;
DR WPI: 1999-480840/41.
DR N-PSDB; AA209170.
XX New insoluble proteins, and fragments, that bind to tumor necrosis
PT factor, used to treat e.g. septic shock or cerebral malaria
XX
XX Claim 4a; Fig 1; 25pp; German.
PS This invention describes novel homogeneous insoluble proteins (I),
CC their (in)soluble fragments (IIa) and their salts that can bind tumour
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (I) and (IIa) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence represents
CC a tumour necrosis factor binding protein described in the method of
CC the invention.
CC (Updated on 20-MAR-2003 to correct PR field.)
CC (Updated on 20-MAR-2003 to correct PR field.)
XX
XX Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 20; Length 455;

Best Local Similarity 62.9%; Pred. No. 1.4e-95;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPGKRYNHPONSTICT 60
DB 1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLGDREKRSVCPGKRYIHPONNISICT 60
QY 61 KCHKGTYLYNDGPGPGDTRDCRVACPGTYTALLENHRLCLSCSRDEMFQVEISPCVVD 120
DB 61 KCHKGTYLYNDGPGPGDTRDCRVACPGTYTALLENHRLCLSCSRDEMFQVEISPCVVD 120
QY 121 RDTVCGCRKNQRYRYWGETGFRCLNCSLCPNGTVNIPCOERODTICCHMGFFLKAKCI 180
DB 121 RDTVCGCRKNQRYRYWSENLFCFCNCSLCNLTNHLSCOEKONTVCTCHAGFFLENECV 180
QY 181 SCHDCKNK-ECEKLCPTRPSTGKSDPGTTLVPLVIVFGICLASPASVVIACRYGRWK 239

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Db 181 SCNNCKSLKCTKCLPQIENVKGTEDSGTTLPLVIFGLCLSLFLIGLMRYQRMK 240
Qy 240 PKLSIIIGOSTLVKEGEPE-----LLVPAQGNP-----TTTICFSSTPSSSPVSIPIYI 290
Db 241 SKLSIVCGKSTPEKEGELTGTTKPLAPNPSFSPFTPLGSPVPSSTFTSSSTYT 300
Qy 291 SCDSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTGPPASTHLCT 350
Db 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATLA-----ASDP1P 335
Qy 351 TPVQKMEASAPASAPDQADADPATLVAVDGVPPSRKMLVRLGLSEHIEIRLENGR 410
Db 336 NPLQKMEASA-HKQOSLDTDDPATLVAVENVPPLRWKEFVRRLGLSDHEIDRLQLNGR 394
Qy 411 HLEAQSMTLAAMRRRTPRREATTELLGRVLRDMDLGCLLENIEBALGGAARLASERPLL 470
Db 395 CLREAOYSMLATWRRRTPRREATTELLGRVLRDMDLGCLLENIEBALGGAARLASERPLL 454

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RESULT 9

AAB36266 ID AAB36266 standard; Protein; 455 AA.

XX AAB36266;

DT 20-FEB-2001 (first entry)

XX Human tumour necrosis factor receptor 1.

XX Human: death domain containing receptor; DR3-VI; cancer;
 KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
 KW neurodegenerative disease; angiogenesis.

XX Homo sapiens.

XX MO200064465-A1.

XX 02-NOV-2000.

XX 21-APR-2000; 2000WO-US10741.

XX 22-APR-1999; 99US-0130488.

XX 28-MAY-1999; 99US-0136741.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (UNMI) UNIV MICHIGAN.

XX (YUGG/) YU G.

XX (NIJJ/) NI J.

XX (GENT/) GENTZ R L.

XX (DILL/) DILLON P J.

XX (DIXI/) DIXIT V M.

XX Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;

XX WPI; 2000-687263/67.

XX Treating graft-versus-host disease, cancer, immunodeficiency or an
 PT autoimmune disease comprising administering an antibody to Death Domain
 PT Containing Receptor proteins and a second therapeutic agent -

XX Disclosure; Fig 3; 273pp; English.

XX The present invention provides the protein and coding sequences for two
 CC death domain containing receptors, designated DR3 and DR3-VI. These
 CC receptors are involved in apoptosis, and the sequences given can be used
 CC in the treatment of cancers, infections, cardiovascular disorders such as
 CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
 CC and congenital heart defects, neurodegenerative diseases including
 CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
 CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
 CC and to promote angiogenesis and wound healing.

SQL Sequence 455 AA:

Query Match 58.3%; Score 1517; DB 21; Length 455;
 Best Local Similarity 62.9%; Pred. No. 1.4e-95;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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Qy 1 MGLPTVRLPLPLPALADVPAGVQGLVPHPGDLKRESPPQGRKYNHPONSTICT 60
Db 1 MGLSTVDPDLLPLLELLELVGIVPSGVIGLPHGLDREKRSVCPQGRKYIHPONNSICT 60
Qy 61 KCHGKTYLVNDCCPGGRDTCRCVAPGTYTALENHLRRCSCSRGPEMPOVEISPCVVD 120
Db 61 KCHKGTLYVNDCCPGQDTCRCBESGFTASENHLRRCSCSRKEMGVEIISCTVD 120
Qy 121 RDTVCGCRKQRYREYWGSETRFCINCSICPNGTVNIPCEERODTICCHMGFFPKGAKCI 180
Db 121 RDTVCGCRKQRYRYWSENLFCQFNCSLCLNGTVHLSQGBQNTVCTCHAGFTLRNECV 180
Qy 181 SCHDCRKN-EGCKLCPTPRSTGSDQPGTTVLLPLVIYFGLCLASPVAVTLACRYQRMK 239
Db 181 SCNNCKSLKCTKCLPQIENVKGTEDSGTTLPLVIFGLCLSLFLIGLMRYQRMK 240
Qy 240 PKLSIIIGOSTLVKEGEPE-----LLVPAQGNP-----TTTICFSSTPSSSPVSIPIYI 290
Db 241 SKLSIVCGKSTPEKEGELTGTTKPLAPNPSFSPFTPLGSPVPSSTFTSSSTYT 300
Qy 291 SCDSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTGPPASTHLCT 350
Db 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATLA-----ASDP1P 335
Qy 351 TPVQKMEASAPASAPDQADADPATLVAVDGVPPSRKMLVRLGLSEHIEIRLENGR 410
Db 336 NPLQKMEDSA-HKQOSLDTDDPATLVAVENVPPLRWKEFVRRLGLSDHEIDRLQLNGR 394
Qy 411 HLEAQSMTLAAMRRRTPRREATTELLGRVLRDMDLGCLLENIEBALGGAARLASERPLL 470
Db 395 CLREAOYSMLATWRRRTPRREATTELLGRVLRDMDLGCLLENIEBALGGAARLASERPLL 454

```

RESULT 10

AAB37800 ID AAB37800 standard; Protein; 455 AA.

XX AAB37800;

DT 23-FEB-2001 (first entry)

XX Human tumour necrosis factor p55 receptor.

XX Human: tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
 KW p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
 KW immunosuppressive; immunomodulator; cardiac; cytoskeletal; cachexia;
 KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
 KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
 KW chronic myelogenous leukaemia; inflammatory bowel disease.

XX Homo sapiens.

XX MO200064479-A1.

XX 02-NOV-2000.

XX 26-APR-2000; 2000WO-US11700.

XX 27-APR-1999; 99US-0301274.

XX (ANT1-) ANTIBODY SYSTEMS INC.

XX Fredeking TM, Ignatjev GM;

XX WPI; 2000-679646/66.

XX Novel compositions comprising tetracycline or tetracycline-like

PT compounds for the treatment and/or prevention of acute inflammatory
PT responses and diseases, e.g. septic shock and immune complex-induced
PT colitis -

XX Disclosure; Page 167-169; 183pp; English.

XX The present sequence is given in a specification relating to novel
XX compositions and methods containing tetracycline or tetracycline-like
XX compounds for treating and/or preventing acute inflammatory responses and
XX diseases. Such diseases include acute inflammatory conditions associated
XX with viral haemorrhagic diseases (including diseases caused by
XX Bunyaviridae, Flaviviridae, or Arenaviridae viruses),
XX parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
XX disorders, acute cardiovascular events, chronic myelogenous leukaemia and
XX transplanted bone marrow-induced graft-versus-host disease, septic shock,
XX immune complex-induced colitis, cerebrospinal fluid inflammation,
XX multiple sclerosis, inflammatory responses associated with trauma,
XX systemic inflammatory response syndrome (SIRS), adult respiratory
XX distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
XX and Crohn's disease.

XX Sequence 455 AA:

Query Match 58.3%; Score 1517; DB 21; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.4e-95;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```

OY 1 MGLPTVPGLLLPLVLPALLADVPYAGVGLVPHRDLEKRESPCGKYNHPONSTICT 60
DB 1 MGLSTVPDLLPLVLLVLELVGIVGLVPHLDREKRSVCPQGVYIHPONNSICT 60
OY 61 KCHKGTLYNDPCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRGRDMFOVEISPCVVD 120
DB 61 KCHKGTLYNDPCPGQDTCRCESGSGFTASBNHLRCLSCSKRKMGOVEISSCTVD 120
OY 121 RDTVCGCRKNQYREYWGTFRCINCSLCPNGTVNI PCQERODTICHGMGFILGAKCI 180
DB 121 RDTVCGCRKNQYRHYWSENLFCFCFNCISCLNGTVHLSQEKQNTVCTCHAGFLAENECV 180
OY 181 SCHDCKNK-BECKLCPTPSTGKSDOPGTTLVPLVIFGLCLASFPASVVLACRYQRMK 239
DB 181 SCNNCKSLKCTKCLPOIENVKGTBDSGTTVLPLVIFGLCLSLFLGIMRYQRMK 240
OY 240 PKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICRSTPSSSPVSIPIYI 290
DB 241 SKLYSIIVCGKSTPEKEGLEGTTRKPLAPNPSFPTPGFTPLGSPVPSSSTFTSYT 300
OY 291 SCDSNFGAVASPSSETAPPHLKAGPILGPPASTHLCTPGPASTHLCTPGPASTHLCT 350
DB 301 PDCPCNF---AAPREVAPPYQADPIL-----ATAL-----ASDPIP 335
OY 351 TPVQKMEASAPADQDLADADPATLYAVVDGVPSPRWKELVRRLGSLSEHIERLENGR 410
DB 336 NPLQWEDSA-HKPSLDLTDPATLYAVVENPPLRWKEFVARLGLSHEIDRLQLONGR 394
OY 411 HUREAOYMLAAMRRTPRBEATLELGRVLRDMPLGLCLENIEBALGAARLASERPL 470
DB 335 CLREAOYMLATWKRTRPRRATLELGRVLRDMPLGLCLBIDBALGAPALPAPASLL 454

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RESULT 11
AAB26984
ID AAB26984 standard; Protein; 455 AA.

XX AAB26984;

XX 02-FEB-2001 (first entry)

XX Human TNFR 1.

XX Human, TNFR 1; tumour necrosis factor; TR9 receptor; immunosuppressive;
XX antiinflammatory; cardiant; antiaesthetic; antidiabetic; antiallergic;
XX antiaesthetic; antineumatic; anti-HIV; anticonvulsant; cytostatic;

KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
KW cardiovascular disease; neurological disease; protein coordinate data.

OS Homo sapiens.

XX WC200056862-A1.

XX 28-SEP-2000.

XX 16-MAR-2000; 2000WO-US06831.

XX 24-MAR-1999; .99US-0126019.

XX 14-MAY-1999; 99US-0134220.

XX (HUMA-1) HUMAN GENOME SCI INC.

XX Ni J, Geniz RL, Yu G, Fan P;

XX WPI; 2000-594575/56.

PT Nucleic acid molecule encoding a human tumor necrosis factor receptor,
PT known as TR9, useful for treating, preventing and diagnosing severe
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
PT and cancer -

XX Disclosure; Fig 2; 220pp; English.

XX The present sequence is TNFR 1, a member of the tumour necrosis factor
XX receptor family. A novel human tumour necrosis factor receptor,
XX designated TR9, has been isolated. The TR9 receptor is also known as
XX Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or
XX agonists are useful for treating, preventing or diagnosing common
XX variable immunodeficiency, X-linked agammaglobulinemia, severe combined
XX immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such
XX as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,
XX diabetes mellitus and asthma), HIV infection, epilepsy, cancer,
XX cardiovascular diseases and other neurological diseases.

XX Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 21; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.4e-95;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```

OY 1 MGLPTVPGLLLPLVLPALLADVPYAGVGLVPHRDLEKRESPCGKYNHPONSTICT 60
DB 1 MGLSTVPDLLPLVLLVLELVGIVGLVPHLDREKRSVCPQGVYIHPONNSICT 60
OY 61 KCHKGTLYNDPCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRGRDMFOVEISPCVVD 120
DB 61 KCHKGTLYNDPCPGQDTCRCESGSGFTASBNHLRCLSCSKRKMGOVEISSCTVD 120
OY 121 RDTVCGCRKNQYREYWGTFRCINCSLCPNGTVNI PCQERODTICHGMGFILGAKCI 180
DB 121 RDTVCGCRKNQYRHYWSENLFCFCFNCISCLNGTVHLSQEKQNTVCTCHAGFLAENECV 180
OY 181 SCHDCKNK-BECKLCPTPSTGKSDOPGTTLVPLVIFGLCLASFPASVVLACRYQRMK 239
DB 181 SCNNCKSLKCTKCLPOIENVKGTBDSGTTVLPLVIFGLCLSLFLGIMRYQRMK 240
OY 240 PKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICRSTPSSSPVSIPIYI 290
DB 241 SKLYSIIVCGKSTPEKEGLEGTTRKPLAPNPSFPTPGFTPLGSPVPSSSTFTSYT 300
OY 291 SCDSNFGAVASPSSETAPPHLKAGPILGPPASTHLCTPGPASTHLCTPGPASTHLCT 350
DB 301 PDCPCNF---AAPREVAPPYQADPIL-----ATAL-----ASDPIP 335
OY 351 TPVQKMEASAPADQDLADADPATLYAVVDGVPSPRWKELVRRLGSLSEHIERLENGR 410

```

Db 336 NPLQKWEBSA-HKQSLDTPDPAVLAVAVENVPPLRWKEFVRLGLSDBEIDRLQNGR 394
 QY 411 HLEBAQYSMLAAMRRRPRRATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPLL 470
 Db 395 CLREBAQYSMLATWRRRTPRRRATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPLL 454

RESULT 12
 AAB23446
 ID AAB23446 standard; Protein; 455 AA.
 AC AAB23446;
 DT 12-JAN-2001 (first entry)
 DE Human tumour necrosis factor receptor 1 protein.
 KW TNFRI; tumour necrosis factor receptor; polymorphism; human;
 KM tumour; cancer; apoptosis; bacterial infection.
 OS Homo sapiens.
 XX MO200050436-A1.
 XX 31-AUG-2000.
 PF 23-FEB-2000; 2000WO-US04606.
 PR 23-FEB-1999; 99US-0121314.
 PA (GENA-) GENAISSANCE PHARM INC.
 PA (NAND/) NANDABALAN K.
 PA (SCHU/) SCHULZ V P.
 PA (STEP/) STEPHENS J C.
 PA (CHEW/) CHEW A.
 PI Mandabalan K, Schulz VP, Stephens JC, Chew A;
 DR WPI; 2000-543909/49.
 DR N-PSDB; AAA95105.

PT Polynucleotides comprising polymorphic variants of a reference sequence for tumour necrosis factor receptor 1 (TNFRI), useful for studying the biological function of TNFRI and identifying drugs targeting the protein for treating disorders -
 PT protein for treating disorders -
 PS Claim 10; Fig 5; 79pp; English.
 CC The present invention relates to polymorphic variants of the tumour necrosis factor receptor 1 (TNFRI) gene. The present sequence is the TNFRI protein. The sequence of the whole gene is given in AAA95102, AAA95103 and AAA95104. The polymorphisms were identified by amplifying and sequencing regions of the gene. Twelve polymorphic loci were discovered. Of these twelve polymorphisms, four can cause a change in the TNFRI protein. The TNFRI polymorphisms may be useful for studying the biological function of TNFRI as well as for identifying drugs targeting the protein for treatment of disorders related to its abnormal expression or function such as tumours, apoptosis related disorders and bacterial infection.

Query Match 58.3%; Score 1517; DB 21; Length 455;
 Best Local Similarity 62.9%; Pred. No. 1,4e-95;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPLLLPLVLPALLAVVYPAGVQSLVPHSPDLKRBSPPCQGYNHPQNSTICT 60
 Db 1 MGLSTVPLLLPLVLPALLAVVYPAGVQSLVPHSPDLKRBSPPCQGYNHPQNSTICT 60
 QY 61 KCHKTYLYNDGPGRQDTDCVCAAGVYTALENHLRCLSCGRCDDEMFOVEISPCVDD 120
 Db 395 CLREBAQYSMLATWRRRTPRRRATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPLL 454

Db 61 KCHKTYLYNDGPGRQDTDCVCAAGVYTALENHLRCLSCGRCDDEMFOVEISPCVDD 120
 QY 121 RDTVCGCRKQNYREYMGTFGRCLNCSLCPMGTVNIPCOERODPTCHGMGFLLGAKCI 180
 Db 121 RDTVCGCRKQNYREYMGTFGRCLNCSLCPMGTVNIPCOERODPTCHGMGFLLGAKCI 180
 QY 181 SCHDCXNK-ECEKLCPTRPSTGKDSODPGITVLLPLVIVFGLCLASFAVVLACRYORWK 239
 Db 181 SCNCKKSLECKTCLPQIENVKGTEDSGTTLPLVIFGLCLLSLFLGLMYRYQWK 240
 QY 240 PKYSLICGOSTLVKEGPE-----LVPAFGPNP-----TTTICPSSPSSSPUSIPYI 290
 Db 241 SKLYSIYCGKSTPKEGELGTTTKPLAPNPSFPTPGFTPLGSPVSSSTFTSSSTYT 300
 QY 291 SCDRSNFGAVASPSSETAPPLKAGPILPGPPASTHLCTPGPPASTHLCTGPPASTHL 350
 Db 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATL-----ASDPIP 335
 QY 351 TPVQKWEASAPSDQADADPAVLAVAVDVPSPRWKELVRLGLSDBEIDRLQNGR 410
 Db 336 NPLQKWEBSA-HKQSLDTPDPAVLAVAVENVPPLRWKEFVRLGLSDBEIDRLQNGR 394
 QY 411 HLEBAQYSMLAAMRRRPRRATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPLL 470
 Db 395 CLREBAQYSMLATWRRRTPRRRATLELLGRVLRDMDLGCLLENIEBALGGAARLASERPLL 454

RESULT 13
 AAB01336
 ID AAB01336 standard; Protein; 455 AA.
 AC AAB01336;
 DT 25-SEP-2000 (first entry)
 DE TNF-R1 death receptor.
 KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus; human.
 OS Homo sapiens.
 XX MO200034335-A2.
 XX 15-JUN-2000.
 PF 03-DEC-1999; 99WO-US26035.
 PR 04-DEC-1998; 98US-0205018.
 PA (SCHB) SCHERING CORP.
 PI Leong C, Phillips JH;
 DR WPI; 2000-423383/36.

PT Purified or recombinant polypeptide for modulating apoptosis comprises a sequence which binds to an antibody specific for U1L4 or its fragments
 PS Disclosure; Page 65-67; 76pp; English.
 CC A pure or recombinant polypeptide which binds to a polyclonal antibody specific for the mature U1L4 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or development, such as cancer or degenerative conditions and for regulation of viral infection and replication. At least five different death receptors are known, which include the CD95 (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated protein (TRAMP), death receptor-6 (DR-6), and TNF-related

CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
 XX Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 21; Length 455;
 Best Local Similarity 62.9%; Pred. No. 1.4e-95;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGDLLPLVLPALLADVPAGVGLVPHRDLERESPCKQKYNHONSTICT 60
 DB 1 MGLSTVPDLPLPLVLELVGIVPSGVGLVPHLDREGRDVSQPKYIHPONNSTICT 60
 QY 61 KCHKGTLYNDPCPGPGRDTCRCVCAPGTYTALENHRLRCLSCSRDEMFVEISPCVD 120
 DB 61 KCHKGTLYNDPCPGPGRDTCRCVCAPGTYTALENHRLRCLSCSRDEMFVEISPCVD 120
 QY 121 RDTVCGCRKNQRYRWYSGETGFRCLNCSLCPNGTVNIPCOERODTICHGMGFLLGAKCI 180
 DB 121 RDTVCGCRKNQRYRWYSGETGFRCLNCSLCPNGTVNIPCOERODTICHGMGFLLGAKCI 180
 QY 181 SCHDCKNK-ECERKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASPAVYLACRYORWK 239
 DB 181 SCNNCKSLKCTKCLPOLIENVKGTEDSGTVLLPLVIFGLCLSLPLGLMRYORWK 240
 QY 240 PKLYSIICGOSTLVKEGPE-----LVPAFGFNP-----TTTICFSSPSSSPVSIPIYI 290
 DB 241 SKLYSIVCGKSTPRKEGELGTTTKPLAPNPSFPTPGPTTLGSPVPSSTFTSSSYT 300
 QY 291 SCDRNFQAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 DB 301 PGDCPNF---AAPREVAPFYOGADPIL-----ATAL-----ASDPIP 335
 QY 351 TPVQKWEASASAPADQLADADPATLYAVNDGVPSPRKLVLRLGLSEHIERLEENGR 410
 DB 336 NPLQKWEESA-HKQOSLDTPDPAITYAVENVPLRKKEFVRRLGLSDHEIDRLQLONGR 394
 QY 411 HLREAOYSMLAAMRRRTPRREATLELGRVLRDMDLGLCLENIEBALGAARLASBPRL 470
 DB 395 CLREAOYSMLATWRRTPRREATLELGRVLRDMDLGLCLENIEBALGPALPPAPBLL 454

RESULT 14
 ID AAB86817 standard; Protein; 455 AA.

AC AAB86817;
 DT 12-NOV-2001 (first entry)
 XX Human TNF α -associated protein #1.
 XX TNF α , tumor necrosis factor binding protein; TNF α ; treatment;
 KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
 KW antiprotococcal; treatment; meningococcal sepsis; cerebral malaria;
 KW autoimmune glomerulonephritis.

OS Homo sapiens.
 XX EPI132471-A2.
 PN 12-SEP-2001.

PF 31-AUG-1990; 2001EP-0108117.
 PR 12-SEP-1989; 88CH-0003319.
 PR 08-MAR-1990; 90CH-0000746.
 PR 20-APR-1990; 90CH-0001347.
 PR 31-AUG-1990; 90EP-0116707.
 PR 31-AUG-1990; 99EP-0100703.

PA (HOPF) HOPFMAN LA ROCHE & CO AG F.
 XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
 FJ

P1 Schlaeger E;
 XX WPI: 2001-559312/63.
 DR N-PSDB; AAB48859.

PT New homogeneous, insoluble proteins that bind tumor necrosis factor
 XX (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
 PS Claim 4a; Fig 1; 26pp; German.

CC This invention describes novel insoluble proteins (I), also their
 CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
 CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
 CC invention have antiinflammatory, immunosuppressive, antibacterial,
 CC antiprotococcal activity (I), and related recombinant proteins, are used
 CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
 CC sepsis, development of autoimmune glomerulonephritis and cerebral
 CC malaria. Also (I), or antibodies specific for them, are used for
 CC diagnostic determination of TNF in body fluids, for affinity purification
 CC of TNF and for identifying (ant)agonists of TNF. This sequence represents
 CC a human TNF binding protein described in the method of the invention.

XX Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 22; Length 455;
 Best Local Similarity 62.9%; Pred. No. 1.4e-95;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGDLLPLVLPALLADVPAGVGLVPHRDLERESPCKQKYNHONSTICT 60
 DB 1 MGLSTVPDLPLPLVLELVGIVPSGVGLVPHLDREGRDVSQPKYIHPONNSTICT 60
 QY 61 KCHKGTLYNDPCPGPGRDTCRCVCAPGTYTALENHRLRCLSCSRDEMFVEISPCVD 120
 DB 61 KCHKGTLYNDPCPGPGRDTCRCVCAPGTYTALENHRLRCLSCSRDEMFVEISPCVD 120
 QY 121 RDTVCGCRKNQRYRWYSGETGFRCLNCSLCPNGTVNIPCOERODTICHGMGFLLGAKCI 180
 DB 121 RDTVCGCRKNQRYRWYSGETGFRCLNCSLCPNGTVNIPCOERODTICHGMGFLLGAKCI 180
 QY 181 SCHDCKNK-ECERKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASPAVYLACRYORWK 239
 DB 181 SCNNCKSLKCTKCLPOLIENVKGTEDSGTVLLPLVIFGLCLSLPLGLMRYORWK 240
 QY 240 PKLYSIICGOSTLVKEGPE-----LVPAFGFNP-----TTTICFSSPSSSPVSIPIYI 290
 DB 241 SKLYSIVCGKSTPRKEGELGTTTKPLAPNPSFPTPGPTTLGSPVPSSTFTSSSYT 300
 QY 291 SCDRNFQAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 DB 301 PGDCPNF---AAPREVAPFYOGADPIL-----ATAL-----ASDPIP 335
 QY 351 TPVQKWEASASAPADQLADADPATLYAVNDGVPSPRKLVLRLGLSEHIERLEENGR 410
 DB 336 NPLQKWEESA-HKQOSLDTPDPAITYAVENVPLRKKEFVRRLGLSDHEIDRLQLONGR 394
 QY 411 HLREAOYSMLAAMRRRTPRREATLELGRVLRDMDLGLCLENIEBALGAARLASBPRL 470
 DB 395 CLREAOYSMLATWRRTPRREATLELGRVLRDMDLGLCLENIEBALGPALPPAPBLL 454

RESULT 15
 ID AAB36697 standard; Protein; 455 AA.

AC AAB36697;
 DT 15-MAR-2001 (first entry)

DE Human tumour necrosis factor receptor TNFR1 protein SEQ ID NO:3.
 XX Human; tumour necrosis factor receptor 5; TR1D; TNFR-5; TR5; noctropic;
 KW TRAIL receptor without intracellular domain; diagnosis; cyostatic;
 XX

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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:03:14 ; Search time 21 Seconds

(without alignments)
948.972 Million cell updates/sec

Title: US-09-970-532-2

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Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1519	58.4	455	4	US-08-406-824A-4
3	1517	58.3	455	1	US-08-321-668-2
4	1517	58.3	455	1	US-08-837-941-2
5	1517	58.3	455	2	US-08-126-016-2
6	1517	58.3	455	3	US-08-815-469-5
7	1517	58.3	455	3	US-09-006-353A-3
8	1517	58.3	455	4	US-09-527-236A-5
9	1517	58.3	455	4	US-08-054-970-2
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11	1517	58.3	455	4	US-09-573-986-3
12	1517	58.3	455	4	US-09-027-287-3
13	1517	58.3	455	1	US-09-253-656B-3
14	1512	58.1	455	1	US-08-050-319B-25
15	1512	58.1	455	2	US-08-465-982-25
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20	1423	54.7	426	4	US-08-747-562-37
21	1072	41.2	281	4	US-09-513-007-4
22	1019	39.1	280	3	US-08-974-022-46
23	1019	39.1	280	3	US-08-795-445A-46
24	1019	39.1	280	3	US-08-795-447A-46
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31	727.5	27.9	336	3	US-08-804-166-8	Sequence 8, Appli
32	727.5	27.9	336	3	US-08-910-991-8	Sequence 8, Appli
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34	719	27.6	167	1	US-08-050-319B-57	Sequence 57, Appli
35	719	27.6	167	2	US-08-465-982-2	Sequence 2, Appli
36	719	27.6	167	2	US-08-465-982-57	Sequence 57, Appli
37	680.5	26.1	285	3	US-08-804-166-6	Sequence 6, Appli
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39	679	26.1	307	3	US-08-804-166-4	Sequence 4, Appli
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41	674.5	25.9	161	4	US-09-326-394-2	Sequence 2, Appli
42	670.5	25.8	153	2	US-08-219-237B-4	Sequence 4, Appli
43	670.5	25.8	153	3	US-08-477-347-12	Sequence 12, Appli
44	670.5	25.8	153	3	US-08-476-862-3	Sequence 3, Appli
45	670.5	25.8	153	3	US-08-468-560C-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-09-513-007-2
; Sequence 2, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kenell, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-016001
; CURRENT APPLICATION NUMBER: US/09/513,007
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/122,156
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ. ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-513-007-2

Query Match      100.0%; Score 2603; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.6e-197;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLPTVGGLLPLVPLALLADVYPAGVQGLVPHPGDLEKESPPCKYHNPONSTICT 60
DB 1 MGLPTVGGLLPLVPLALLADVYPAGVQGLVPHPGDLEKESPPCKYHNPONSTICT 60
QY 61 KCHKGTLYNDPCPGBDTCRCVAPGTYALENHLRRCSCSCKREMFQVEISPCVVD 120
DB 61 KCHKGTLYNDPCPGBDTCRCVAPGTYALENHLRRCSCSCKREMFQVEISPCVVD 120
QY 121 RDTVCGGRKQVREYMGTFRCINCSLCPNGTVNI PQERODTICHNGFPLKAKCI 180
DB 121 RDTVCGGRKQVREYMGTFRCINCSLCPNGTVNI PQERODTICHNGFPLKAKCI 180
QY 181 SCHDCKKKECKCPTRPSTGKSDPGTIVLPLVVFELCLASFASVVLACRYQWKRP 240
DB 181 SCHDCKKKECKCPTRPSTGKSDPGTIVLPLVVFELCLASFASVVLACRYQWKRP 240
QY 241 KLVSIIGQSTLVKEGPELVLPAPGNPTTICFSSTPSSPVSTIPYISCDRSNFGAV 300
DB 241 KLVSIIGQSTLVKEGPELVLPAPGNPTTICFSSTPSSPVSTIPYISCDRSNFGAV 300
QY 301 ASRSSETAPHLKAGPLPGPPASTHLCTGPASTHLCTGPASTHLCTPVQKWEASA 360
DB 301 ASRSSETAPHLKAGPLPGPPASTHLCTGPASTHLCTGPASTHLCTPVQKWEASA 360

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Db 301 ASPSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPGVQKWEASA 360
Qy 361 PSAPQGLADAPATYAVVDGVPSPRKEVLRRGLSEHEIERLENGRHLREAOYSL 420
Db 361 PSAPQGLADAPATYAVVDGVPSPRKEVLRRGLSEHEIERLENGRHLREAOYSL 420
Qy 421 AAMRRRTTREATLELGRVLDMDLGLCLENIEBALGAARLASERPLW 471
Db 421 AAMRRRTTREATLELGRVLDMDLGLCLENIEBALGAARLASERPLW 471

RESULT 2
US-08-406-824A-4
Sequence 4, Application US/08406824A
Patent No. 6541610

GENERAL INFORMATION:
APPLICANT: SMITH, Craig A.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
FILE REFERENCE: A-71592
CURRENT APPLICATION NUMBER: US/08/406,824A
CURRENT FILING DATE: 1995-03-20
PRIOR APPLICATION NUMBER: US 08/255,849
PRIOR FILING DATE: 1994-06-08
PRIOR APPLICATION NUMBER: US 07/860,710
PRIOR FILING DATE: 1992-03-30
PRIOR APPLICATION NUMBER: US 07/523,635
PRIOR FILING DATE: 1990-05-10
PRIOR APPLICATION NUMBER: US 07/421,417
PRIOR FILING DATE: 1989-10-13
PRIOR APPLICATION NUMBER: US 07/405,370
PRIOR FILING DATE: 1989-09-11
PRIOR APPLICATION NUMBER: US 07/403,241
PRIOR FILING DATE: 1988-09-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 4
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-08-406-824A-4

Query Match 58.4%; Score 1519; DB 4; Length 455;
Best Local Similarity 62.9%; Pred. No. 1e-111;
Matches 302; Conservative 39; Mismatches 103; Indels 36; Gaps 7;

Qy 1 MGLPTVPGLLPLVLPALADYPRAGVGLVPHRGLREKRESPCQKKNHPQNSTICT 60
Db 1 MGLSTVPDLLPLVLELVLGIVPSGVGLVPHLDREKRDVCPQGXKIHPONNISICT 60
Qy 61 KCHKGTLYNDCPGGRDTCRVCAAGTYTALENHLRCLSCSRCDENFQVEISPCVVD 120
Db 61 KCHKGTLYNDCPGGRDTCRVCAAGTYTALENHLRCLSCSRCDENFQVEISPCVVD 120
Qy 121 RDTVCGCRKNQYREYVGTGFRCLNCSLCPNGTVNI PCQERODIT CHCHMGFFLGAKCI 180
Db 121 RDTVCGCRKNQYRHVWSENLFCFCNCSLCLNGTVHLSQCKKNTVCTGAGFFLENECV 180
Qy 181 SCHDCKNK-ECBKLCPTBPSTGKSDODPGTIVLLPLVIVFGICLASFASVVLACYORWK 239
Db 181 SCHDCKNK-ECBKLCPTBPSTGKSDODPGTIVLLPLVIVFGICLASFASVVLACYORWK 239
Qy 240 PLYYSIIICQSTVLVEGEPE-----LLVPAQGNP-----TTTICSPSPSSSPVSIPIYI 290
Db 240 PLYYSIIICQSTVLVEGEPE-----LLVPAQGNP-----TTTICSPSPSSSPVSIPIYI 290
Qy 291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
Db 301 PGDCRNF---AARREVPAPYOGADPIL-----ATL-----ASDPIP 335
Qy 351 TPVQKWEASAPAPQGLADAPATYAVVDGVPSPRKEVLRRGLSEHEIERLENGRHL 410
Db 351 TPVQKWEASAPAPQGLADAPATYAVVDGVPSPRKEVLRRGLSEHEIERLENGRHL 410
Qy 361 NPLQKWEBSA-HKPGSLDTPDDPATYAVVENVPRLKWEKFEVRLGLSDHEIRLENGR 394
Db 361 NPLQKWEBSA-HKPGSLDTPDDPATYAVVENVPRLKWEKFEVRLGLSDHEIRLENGR 394

Qy 411 HLRQOYSLMAAMRRRTTREATLELGRVLDMDLGLCLENIEBALGAARLASERPL 470
Db 395 CLRQOYSLMAAMRRRTTREATLELGRVLDMDLGLCLENIEBALGAARLASERPL 454

RESULT 3
US-08-321-668-2
Sequence 2, Application US/08321668
Patent No. 565859

GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARPOLOMEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-321-668-2

Query Match 58.3%; Score 1517; DB 1; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGLLPLVLPALADYPRAGVGLVPHRGLREKRESPCQKKNHPQNSTICT 60
Db 1 MGLSTVPDLLPLVLELVLGIVPSGVGLVPHLDREKRDVCPQGXKIHPONNISICT 60
Qy 61 KCHKGTLYNDCPGGRDTCRVCAAGTYTALENHLRCLSCSRCDENFQVEISPCVVD 120
Db 61 KCHKGTLYNDCPGGRDTCRVCAAGTYTALENHLRCLSCSRCDENFQVEISPCVVD 120
Qy 121 RDTVCGCRKNQYREYVGTGFRCLNCSLCPNGTVNI PCQERODIT CHCHMGFFLGAKCI 180
Db 121 RDTVCGCRKNQYRHVWSENLFCFCNCSLCLNGTVHLSQCKKNTVCTGAGFFLENECV 180
Qy 181 SCHDCKNK-ECBKLCPTBPSTGKSDODPGTIVLLPLVIVFGICLASFASVVLACYORWK 239
Db 181 SCHDCKNK-ECBKLCPTBPSTGKSDODPGTIVLLPLVIVFGICLASFASVVLACYORWK 239
Qy 240 PLYYSIIICQSTVLVEGEPE-----LLVPAQGNP-----TTTICSPSPSSSPVSIPIYI 290
Db 240 PLYYSIIICQSTVLVEGEPE-----LLVPAQGNP-----TTTICSPSPSSSPVSIPIYI 290

Db 241 SKLSIVCGKSTPEKEGELGTTTKPLAPNPSFSTPGFTPLIGSPVSSSTFTSSSTYT 300
Qy 291 SCDSNFGAVASPSSEETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
Db 301 PGDCPNF---AAPREVAPFYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVOKMEASAPASPDOLADPATLVAVDGVPSPRWKELVRLGSEHEIERLEENGR 410
Db 336 NPLQKMEDSA-HKPOSIDTDPPATLVAVENVPPLRWKELVRLGSEHEIERLEENGR 394
Qy 411 HREAOYSMLAARRRTPREATELIGRVLARDMDLGCLENIEBALGGAARLASERPL 470
Db 395 CLRBAQSMLATYRRRTPRREATELIGRVLARDMDLGCLENIEBALGGAARLASERPL 454

RESULT 4
US-08-837-941-2
Sequence 2, Application US/08837941
Patent No. 576917

GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARPOLOMEY, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,941
FILING DATE: 28-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,668
FILING DATE: 12-OCT-1994

APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=13

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 455 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-837-941-2

Query Match 58.3%; Score 1517; DB 1; Length 455;
Best Match Similarity 62.9%; Pred. No. 1.5e-11;
Matches 302; Conservative 36; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGALLPLVLPALLADVPAGVQGLVPHPGDLEKESPCQKYNHPQNSTICTCT 60
Db 1 MGLSTVDDLPLPLVLTLLVGLVYSVIGLVPHLGDREKSDSVCPQKXTHPNQNSICTCT 60

Qy 61 KCHKGYLVNDCCPGGRDTCRVACPGTYTALLENHLRCLSCGRCDREMFQVEISPCVVD 120
Db 61 KCHKGYLVNDCCPGGRDTCRVACPGTYTALLENHLRCLSCGRCDREMFQVEISPCVVD 120
Qy 121 RDTVCGGRKQYRYRWETGRCLNCSLCVNGTNNICQERODTICCHNGFFLKAKCI 180
Db 121 RDTVCGGRKQYRYRWETGRCLNCSLCVNGTNNICQERODTICCHNGFFLKAKCI 180
Qy 181 SCHDCRKR-SCERKLCPRPSTGKDSODPGTTVLPLVTVGLCLASVASVLAQRYRWK 239
Db 181 SCHDCRKR-SCERKLCPRPSTGKDSODPGTTVLPLVTVGLCLASVASVLAQRYRWK 239
Qy 240 PKVSIICGOSTLVKEGPE-----LLVPAGFNP-----TTTCFSSTPSSPVSIPIYI 290
Db 241 SKLSIVCGKSTPEKEGELGTTTKPLAPNPSFSTPGFTPLIGSPVSSSTFTSSSTYT 300
Qy 291 SCDSNFGAVASPSSEETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
Db 301 PGDCPNF---AAPREVAPFYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVOKMEASAPASPDOLADPATLVAVDGVPSPRWKELVRLGSEHEIERLEENGR 410
Db 336 NPLQKMEDSA-HKPOSIDTDPPATLVAVENVPPLRWKELVRLGSEHEIERLEENGR 394
Qy 411 HREAOYSMLAARRRTPREATELIGRVLARDMDLGCLENIEBALGGAARLASERPL 470
Db 395 CLRBAQSMLATYRRRTPRREATELIGRVLARDMDLGCLENIEBALGGAARLASERPL 454

RESULT 5
US-08-126-016-2
Sequence 2, Application US/08126016
Patent No. 581261

GENERAL INFORMATION:
APPLICANT: WALLACH, DAVID
APPLICANT: MOPHER, YARON
APPLICANT: KEMPER, OLIVER
APPLICANT: ENGELMANN, HARTMUT
APPLICANT: BRAKEBUSCH, CORD
APPLICANT: ADERKA, DAN

TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,016
FILING DATE: 24-SEP-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.

REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 455 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-126-016-2

Query Match 58.3%; Score 1517; DB 2; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-11;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPDLPLPLVLPALLADVPAGVGLVPHGDLKRSPPCGKYNHPONSTICT 60
DB 1 MGLSTVPDLPLPLVLELVGLVIGVGLVPHGLDREKRSVCPQKTHPNNISICT 60
DB 61 KCHKGTLYNDCPGRGDTPDCRCVCAAGTYTALENHLRCLSCSRDRDMPQVEISPCVVD 120
DB 61 KCHKGTLYNDCPGRGDTPDCRCVCAAGTYTALENHLRCLSCSRDRDMPQVEISPCVVD 120
QY 121 RDTVCGCRKNQRYEYWGTEGFRCLNCSLCPNGTVNI PCQERODTI CHCMGFPLGAKCI 180
DB 121 RDTVCGCRKNQRYEYWGTEGFRCLNCSLCPNGTVNI PCQERODTI CHCMGFPLGAKCI 180
QY 181 SCHDCKNK-ECEKLCPTRPSTGKSDQDPGTTLVLPVIVFGCLCLASFASVVLACYORWK 239
DB 181 SCNCKKSLBCTKCLPQIENKGTEDSGTTLVLPVIVFGCLCLSLFLIGLMRYQRMK 240
QY 240 PLYSIIIGQSTLVKEGEPE-----LVVAPGFNP-----TTTICFSSPTSSSPVSIPIYI 290
DB 241 SKLVSIVCGKSTPEKEGLEGTTTTPPLANPSFSPTPGTPTLIGSPVPSSTFTSSSTYT 300
QY 291 SCDRSNFGAVASPSSEETAAPHLKAGPILPGPASTHLCTPGPASTHLCTPGPASTHLCT 350
DB 301 PGDCPNF---AAPRRVAPPYOGADPIL-----ATAL-----ASDPIIP 335
QY 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPKWEKELVRRLGLSHEIRLELNGR 410
DB 336 NPLQWMEBSA-HKPSGLTDDPATLYAVVENVPPLRWEKFEVRLGLSHEIRLELNGR 394
QY 411 HUREAOYMLAAMRRTRRREATTLELGRVLRDMDLGLCLENIEBALGAARLASEPRIL 470
DB 395 CLREAOYMLATWRRTTRRREATTLELGRVLRDMDLGLCLENIEBALGAARLASEPRIL 454

RESULT 6
US-08-815-469-5
Sequence 5, Application US/08815469

GENERAL INFORMATION:
PATENT NO. 6153402
APPLICANT: YU, GUO-LIANG
APPLICANT: NI, JIAN
APPLICANT: DIXIE, VIAGRA
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO. 6153402 Yec Assigned
FILING DATE: 06-FEB-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-815-469-5

Query Match 58.3%; Score 1517; DB 3; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-11;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPDLPLPLVLPALLADVPAGVGLVPHGDLKRSPPCGKYNHPONSTICT 60
DB 1 MGLSTVPDLPLPLVLELVGLVIGVGLVPHGLDREKRSVCPQKTHPNNISICT 60
DB 61 KCHKGTLYNDCPGRGDTPDCRCVCAAGTYTALENHLRCLSCSRDRDMPQVEISPCVVD 120
DB 61 KCHKGTLYNDCPGRGDTPDCRCVCAAGTYTALENHLRCLSCSRDRDMPQVEISPCVVD 120
QY 121 RDTVCGCRKNQRYEYWGTEGFRCLNCSLCPNGTVNI PCQERODTI CHCMGFPLGAKCI 180
DB 121 RDTVCGCRKNQRYEYWGTEGFRCLNCSLCPNGTVNI PCQERODTI CHCMGFPLGAKCI 180
QY 121 RDTVCGCRKNQRYEYWGTEGFRCLNCSLCPNGTVNI PCQERODTI CHCMGFPLGAKCI 180
DB 121 RDTVCGCRKNQRYEYWGTEGFRCLNCSLCPNGTVNI PCQERODTI CHCMGFPLGAKCI 180
QY 181 SCHDCKNK-ECEKLCPTRPSTGKSDQDPGTTLVLPVIVFGCLCLASFASVVLACYORWK 239
DB 181 SCNCKKSLBCTKCLPQIENKGTEDSGTTLVLPVIVFGCLCLSLFLIGLMRYQRMK 240
QY 240 PLYSIIIGQSTLVKEGEPE-----LVVAPGFNP-----TTTICFSSPTSSSPVSIPIYI 290
DB 241 SKLVSIVCGKSTPEKEGLEGTTTTPPLANPSFSPTPGTPTLIGSPVPSSTFTSSSTYT 300
QY 291 SCDRSNFGAVASPSSEETAAPHLKAGPILPGPASTHLCTPGPASTHLCTPGPASTHLCT 350
DB 301 PGDCPNF---AAPRRVAPPYOGADPIL-----ATAL-----ASDPIIP 335
QY 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPKWEKELVRRLGLSHEIRLELNGR 410
DB 336 NPLQWMEBSA-HKPSGLTDDPATLYAVVENVPPLRWEKFEVRLGLSHEIRLELNGR 394
QY 411 HUREAOYMLAAMRRTRRREATTLELGRVLRDMDLGLCLENIEBALGAARLASEPRIL 470
DB 395 CLREAOYMLATWRRTTRRREATTLELGRVLRDMDLGLCLENIEBALGAARLASEPRIL 454

RESULT 7
US-09-006-353A-3
Sequence 3, Application US/09006353A

GENERAL INFORMATION:
PATENT NO. 6261801
APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006.353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PP341
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-006-353A-3

Query Match 58.3%; Score 1517; DB 3; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;
QY 1 MGLPTVPGLLPLVLPALLADVPAGVGVLPHPGDLKRESPPCGKYNHPNSTICT 60
DB 1 MGLSTVPGLLPLVLPALLADVPAGVGVLPHPGDLKRESPPCGKYNHPNSTICT 60
QY 61 KCHKGTLYNDPCPGGRDTCRCVAPGTYYALBNHARRCLSCSRCDMFOVEISPCVD 120
DB 61 KCHKGTLYNDPCPGGRDTCRCVAPGTYYALBNHARRCLSCSRCDMFOVEISPCVD 120
QY 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCEORODTCHCHMGFFLGAKCI 180
DB 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCEORODTCHCHMGFFLGAKCI 180
QY 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCEORODTCHCHMGFFLGAKCI 180
DB 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCEORODTCHCHMGFFLGAKCI 180
QY 181 SCHDCNKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLSLFLIGLMTRYQRMK 239
DB 181 SCHDCNKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLSLFLIGLMTRYQRMK 239
QY 240 PKLYSIICGQSTLVKEGPE-----LIVAPGFNP-----TTTICFSTPSSSPVSIPIYI 290
DB 240 PKLYSIICGQSTLVKEGPE-----LIVAPGFNP-----TTTICFSTPSSSPVSIPIYI 290
QY 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFSTPGFTPLGFSPPVSSFTSSSTYT 300
DB 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFSTPGFTPLGFSPPVSSFTSSSTYT 300
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
DB 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
QY 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATL-----ASDPIP 335
QY 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRLGISEHEIRLENGR 410
DB 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRLGISEHEIRLENGR 410
QY 336 NPLQWEDSA-HKPSLTDTPATLYAVVENVPPLRWKEFVRRLGDSHEIDRLQLONGR 394
DB 336 NPLQWEDSA-HKPSLTDTPATLYAVVENVPPLRWKEFVRRLGDSHEIDRLQLONGR 394
QY 411 HLEKQVSMLAMARRTPREATTLELGRVLRDMDLGLCLENIEBALGGAARLASPRLL 470
DB 411 HLEKQVSMLAMARRTPREATTLELGRVLRDMDLGLCLENIEBALGGAARLASPRLL 470
QY 395 CLREKQVSMLATWRRTRPREATTLELGRVLRDMDLGLCLENIEBALGGAARLASPRLL 454
DB 395 CLREKQVSMLATWRRTRPREATTLELGRVLRDMDLGLCLENIEBALGGAARLASPRLL 454

RESULT 8
US-09-527-236A-5
Sequence 5, Application US/09527236A
Patent No. 6358508
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: YU, Guo-Liang

APPLICANT: Fan, Ping
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PR375P1
CURRENT APPLICATION NUMBER: US/09/527.236A
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-527-236A-5

Query Match 58.3%; Score 1517; DB 4; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;
QY 1 MGLPTVPGLLPLVLPALLADVPAGVGVLPHPGDLKRESPPCGKYNHPNSTICT 60
DB 1 MGLSTVPGLLPLVLPALLADVPAGVGVLPHPGDLKRESPPCGKYNHPNSTICT 60
QY 61 KCHKGTLYNDPCPGGRDTCRCVAPGTYYALBNHARRCLSCSRCDMFOVEISPCVD 120
DB 61 KCHKGTLYNDPCPGGRDTCRCVAPGTYYALBNHARRCLSCSRCDMFOVEISPCVD 120
QY 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCEORODTCHCHMGFFLGAKCI 180
DB 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCEORODTCHCHMGFFLGAKCI 180
QY 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCEORODTCHCHMGFFLGAKCI 180
DB 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCEORODTCHCHMGFFLGAKCI 180
QY 181 SCHDCNKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLSLFLIGLMTRYQRMK 239
DB 181 SCHDCNKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLSLFLIGLMTRYQRMK 239
QY 240 PKLYSIICGQSTLVKEGPE-----LIVAPGFNP-----TTTICFSTPSSSPVSIPIYI 290
DB 240 PKLYSIICGQSTLVKEGPE-----LIVAPGFNP-----TTTICFSTPSSSPVSIPIYI 290
QY 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFSTPGFTPLGFSPPVSSFTSSSTYT 300
DB 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFSTPGFTPLGFSPPVSSFTSSSTYT 300
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
DB 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
QY 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATL-----ASDPIP 335
QY 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRLGISEHEIRLENGR 410
DB 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRLGISEHEIRLENGR 410
QY 336 NPLQWEDSA-HKPSLTDTPATLYAVVENVPPLRWKEFVRRLGDSHEIDRLQLONGR 394
DB 336 NPLQWEDSA-HKPSLTDTPATLYAVVENVPPLRWKEFVRRLGDSHEIDRLQLONGR 394
QY 411 HLEKQVSMLAMARRTPREATTLELGRVLRDMDLGLCLENIEBALGGAARLASPRLL 470
DB 411 HLEKQVSMLAMARRTPREATTLELGRVLRDMDLGLCLENIEBALGGAARLASPRLL 470
QY 395 CLREKQVSMLATWRRTRPREATTLELGRVLRDMDLGLCLENIEBALGGAARLASPRLL 454
DB 395 CLREKQVSMLATWRRTRPREATTLELGRVLRDMDLGLCLENIEBALGGAARLASPRLL 454

RESULT 9
US-08-054-970-2
Sequence 2, Application US/08054970
Patent No. 6395267
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKESBUSH, Cord
TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: BROMDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.


```

/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/054,970
/ FILING DATE: 03-MAY-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: WALLACH=9
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 455 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-054-970-2

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Query Match 58.3%; Score 1517; DB 4; Length 455;
Beet Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
DB 1 MGLSTVPLLLPLVLELLVGLVPSGVIGLVPHLDREGRDVSVCQKIHQNNISICT 60
QY 61 KHKGTLYLNDPCPGQRTDRCVCAFGTYTALLENHRLRCLSCSRCDMPQVEISPCVVD 120
DB 61 KHKGTLYLNDPCPGQRTDRCVCAFGTYTALLENHRLRCLSCSRCDMPQVEISPCVVD 120
QY 121 RDTVGGCRKNQRYRHYWSENLFCFNCISLCNGTVHLSCEKQNTVCTCHAGFFLRENECV 180
DB 121 RDTVGGCRKNQRYRHYWSENLFCFNCISLCNGTVHLSCEKQNTVCTCHAGFFLRENECV 180
QY 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTYVLPLVIFGLCLASFASVVLACRYQRMK 239
DB 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTYVLPLVIFGLCLASFASVVLACRYQRMK 239
QY 240 PKLYSIICGQSTLVKEGPE-----LIVPAGFNP-----TTTICFSSTPSSSPVSIPIYI 290
DB 240 PKLYSIICGQSTLVKEGPE-----LIVPAGFNP-----TTTICFSSTPSSSPVSIPIYI 290
QY 291 SCDNSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPPPASTHLCTPPPASTHLCT 350
DB 291 SCDNSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPPPASTHLCTPPPASTHLCT 350
QY 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
QY 351 TPVQKWEASAPASAPDOLADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLEENGR 410
DB 351 TPVQKWEASAPASAPDOLADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLEENGR 410
QY 336 NPLOKWEDESA-HKPGSLDTPDPAITLYAVVENPPLRWKEFVRRLGLSHEIERLEENGR 394
DB 336 NPLOKWEDESA-HKPGSLDTPDPAITLYAVVENPPLRWKEFVRRLGLSHEIERLEENGR 394
QY 411 HLREAYSMLAAMRRRTPRREATLELLGRVLRMDMLGCLLENIEALGGAARLASPEPLL 470
DB 411 HLREAYSMLAAMRRRTPRREATLELLGRVLRMDMLGCLLENIEALGGAARLASPEPLL 470
QY 395 CLREAYSMLATWRRTPRREATLELLGRVLRMDMLGCLLENIEALGGAARLASPEPLL 454
DB 395 CLREAYSMLATWRRTPRREATLELLGRVLRMDMLGCLLENIEALGGAARLASPEPLL 454

```

RESULT 10
US-09-565-916-4

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/ Sequence 4, Application US/09565918
/ Patent No. 6433147
/ GENERAL INFORMATION:
/ APPLICANT: Ni, Jian
/ APPLICANT: Roosen, Craig A.
/ APPLICANT: Pan, James G.
/ APPLICANT: Gentz, Reiner L.

```

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/ APPLICANT: Dixit, Viahva M.
/ TITLE OF INVENTION: Death Domain Containing Receptor 4
/ FILE REFERENCE: 1488.130005
/ CURRENT APPLICATION NUMBER: US/09/565,918
/ CURRENT FILING DATE: 2000-05-05
/ PRIOR APPLICATION NUMBER: US 60/132,922
/ PRIOR FILING DATE: 1999-05-06
/ PRIOR APPLICATION NUMBER: US 09/013,895
/ PRIOR FILING DATE: 1998-01-27
/ PRIOR APPLICATION NUMBER: US 60/037,829
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: US 60/035,722
/ PRIOR FILING DATE: 1997-01-28
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-565-916-4

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Query Match 58.3%; Score 1517; DB 4; Length 455;
Beet Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
DB 1 MGLSTVPLLLPLVLELLVGLVPSGVIGLVPHLDREGRDVSVCQKIHQNNISICT 60
QY 61 KHKGTLYLNDPCPGQRTDRCVCAFGTYTALLENHRLRCLSCSRCDMPQVEISPCVVD 120
DB 61 KHKGTLYLNDPCPGQRTDRCVCAFGTYTALLENHRLRCLSCSRCDMPQVEISPCVVD 120
QY 121 RDTVGGCRKNQRYRHYWSENLFCFNCISLCNGTVHLSCEKQNTVCTCHAGFFLRENECV 180
DB 121 RDTVGGCRKNQRYRHYWSENLFCFNCISLCNGTVHLSCEKQNTVCTCHAGFFLRENECV 180
QY 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTYVLPLVIFGLCLASFASVVLACRYQRMK 239
DB 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTYVLPLVIFGLCLASFASVVLACRYQRMK 239
QY 240 PKLYSIICGQSTLVKEGPE-----LIVPAGFNP-----TTTICFSSTPSSSPVSIPIYI 290
DB 240 PKLYSIICGQSTLVKEGPE-----LIVPAGFNP-----TTTICFSSTPSSSPVSIPIYI 290
QY 291 SCDNSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPPPASTHLCTPPPASTHLCT 350
DB 291 SCDNSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPPPASTHLCTPPPASTHLCT 350
QY 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
QY 351 TPVQKWEASAPASAPDOLADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLEENGR 410
DB 351 TPVQKWEASAPASAPDOLADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLEENGR 410
QY 336 NPLOKWEDESA-HKPGSLDTPDPAITLYAVVENPPLRWKEFVRRLGLSHEIERLEENGR 394
DB 336 NPLOKWEDESA-HKPGSLDTPDPAITLYAVVENPPLRWKEFVRRLGLSHEIERLEENGR 394
QY 411 HLREAYSMLAAMRRRTPRREATLELLGRVLRMDMLGCLLENIEALGGAARLASPEPLL 470
DB 411 HLREAYSMLAAMRRRTPRREATLELLGRVLRMDMLGCLLENIEALGGAARLASPEPLL 470
QY 395 CLREAYSMLATWRRTPRREATLELLGRVLRMDMLGCLLENIEALGGAARLASPEPLL 454
DB 395 CLREAYSMLATWRRTPRREATLELLGRVLRMDMLGCLLENIEALGGAARLASPEPLL 454

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RESULT 11
US-09-573-986-3

```

/ Sequence 3, Application US/09573986
/ Patent No. 6455040
/ GENERAL INFORMATION:
/ APPLICANT: Wei, Ying-Fei
/ APPLICANT: Ni, Jian
/ APPLICANT: Gentz, Reiner
/ APPLICANT: Ruben, Steven
/ TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
/ FILE REFERENCE: 1488.1280004
/ CURRENT APPLICATION NUMBER: US/09/573,986
/ CURRENT FILING DATE: 2000-05-18
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: Patentin Ver. 2.1

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SEQ ID NO 3
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-573-986-3

Query Match 58.3%; Score 1517; DB 4; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPLLLPLVLPALLADVPYAGVGLVPHGDLKRESPPQCKYKNPNSTICT 60
DB 1 MGLSTVPLLLPLVLLBLVGIYPSGVIGLVPHGLDRKRSVCPQCKYHPNNSICT 60
QY 61 KCHKGTLYNDPCPGRDTCRCVACGTYYALBNHLRRLCSGRDMPQVEISPCVVD 120
DB 61 KCHKGTLYNDPCPGRDTCRCVACGTYYALBNHLRRLCSGRDMPQVEISPCVVD 120
QY 121 RDTVCGCKNOYRBYWGTGRCLNCSLCPRGTNNIPQERODTCHCHMGFPLKAGCI 180
DB 121 RDTVCGCKNOYRBYWGTGRCLNCSLCPRGTNNIPQERODTCHCHMGFPLKAGCI 180
QY 181 SCHDCKNK-ECEKLCPTPSTGKSDOPDGTTLPLVIVFGLCLASFASVVLACRYGRMK 239
DB 181 SCNCKSLECKTCLPQIENVKGTEDSGTTLPLVIFGLCLSLFLIGLMTRYGRMK 240
QY 240 PKLYSIICGOSTLYKEGPE-----LVVAPGPNP-----TTTICSTPSSSPVSIPIYI 290
DB 241 SKLYSIVCGKSTPEKEGELBGTITKPLAPNPSFSPPTPGFTPLGFSVPSSSTFTSSTYT 300
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
DB 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATAL-----ASDPIP 335
QY 351 TPVQKESASAPADQLADADPATLYAVVDGVPSPRMKELVRRLGSLSHEIERLELNGR 410
DB 336 NPLOKMEISA-HKQSLDTPDPAITYAVENVPPRLKMEFARRGLDSHEIDRLQLONGR 394
QY 411 HUREAOYMLAAMRRRTPRREATTLELLGRVLRDMDLGLCLNIEBALGGAARLASEPRL 470
DB 395 CLREAOYMLATWRRRTPRREATTLELLGRVLRDMDLGLCLNIEBALGGAARLASEPRL 454

RESULT 12
US-09-027-287-3
Sequence 3, Application US/09027287A

GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ullrich, Stephen
TITLE OF INVENTION: Apoptosis Inducing Molecule II
FILE REFERENCE: 1488.0650004
CURRENT APPLICATION NUMBER: US/09/027,287A
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 09/003,886
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 08/822,953
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/030,157
PRIOR FILING DATE: 1996-10-31
PRIOR APPLICATION NUMBER: US 60/013,923
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-027-287-3

Query Match 58.3%; Score 1517; DB 4; Length 455;

Best Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPLLLPLVLPALLADVPYAGVGLVPHGDLKRESPPQCKYKNPNSTICT 60
DB 1 MGLSTVPLLLPLVLLBLVGIYPSGVIGLVPHGLDRKRSVCPQCKYHPNNSICT 60
QY 61 KCHKGTLYNDPCPGRDTCRCVACGTYYALBNHLRRLCSGRDMPQVEISPCVVD 120
DB 61 KCHKGTLYNDPCPGRDTCRCVACGTYYALBNHLRRLCSGRDMPQVEISPCVVD 120
QY 121 RDTVCGCKNOYRBYWGTGRCLNCSLCPRGTNNIPQERODTCHCHMGFPLKAGCI 180
DB 121 RDTVCGCKNOYRBYWGTGRCLNCSLCPRGTNNIPQERODTCHCHMGFPLKAGCI 180
QY 181 SCHDCKNK-ECEKLCPTPSTGKSDOPDGTTLPLVIVFGLCLASFASVVLACRYGRMK 239
DB 181 SCNCKSLECKTCLPQIENVKGTEDSGTTLPLVIFGLCLSLFLIGLMTRYGRMK 240
QY 240 PKLYSIICGOSTLYKEGPE-----LVVAPGPNP-----TTTICSTPSSSPVSIPIYI 290
DB 241 SKLYSIVCGKSTPEKEGELBGTITKPLAPNPSFSPPTPGFTPLGFSVPSSSTFTSSTYT 300
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
DB 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATAL-----ASDPIP 335
QY 351 TPVQKESASAPADQLADADPATLYAVVDGVPSPRMKELVRRLGSLSHEIERLELNGR 410
DB 336 NPLOKMEISA-HKQSLDTPDPAITYAVENVPPRLKMEFARRGLDSHEIDRLQLONGR 394
QY 411 HUREAOYMLAAMRRRTPRREATTLELLGRVLRDMDLGLCLNIEBALGGAARLASEPRL 470
DB 395 CLREAOYMLATWRRRTPRREATTLELLGRVLRDMDLGLCLNIEBALGGAARLASEPRL 454

RESULT 13
US-09-252-656B-3
Sequence 3, Application US/09252656B

GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Zhang, Jun
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.0650006
CURRENT APPLICATION NUMBER: US/09/252,656B
PRIOR FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: US 60/075,409
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 09/027,287
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 09/003,886
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 08/822,953
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/013,923
PRIOR FILING DATE: 1996-03-22
PRIOR APPLICATION NUMBER: US 60/030,157
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-252-656B-3

Query Match 58.3%; Score 1517; DB 4; Length 455;
Best Local Similarity 62.9%; Pred. No. 1.5e-111;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```

QY 1 MGLPTVPGILLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
DB 1 MGLSTVPDLILLPLVLELVGIYPSGVIGLVPHLADREKRDSDVCPQKXIHPONNISICT 60
QY 61 KCHKGTLYNDCPGRGDTDCRCVCAFGTYTALLENHRLCSGRCDMPFOVEISPCVVD 120
DB 61 KCHKGTLYNDCPGRGDTDCRCESGSGFTASENHLRCLSCSKRKMGOVEISSCTVD 120
QY 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCOERODTICHMGFFLGAKCI 180
DB 121 RDTVCGCRKNQYRHYMSENLFCQCFNCSLCLNGTVHLSQEKONTVCTCHAGFFLAENECV 180
QY 181 SCHDCKK-EECKLCPTPSTGKSDODPGTTLVLPVIVFGICLASFASVVLACYORWK 239
DB 181 SCNCKKSLBECTKCLPQIENVKGTEDSGTTLVLPVIFFGICLLSLFIFGLMYRYORWK 240
QY 240 PLYSIIIGQSTLVKEGPE-----LVPAFGFNP-----TTTICPSSTPSSSPVSIPIYI 290
DB 241 SKLVSIVCGKSTPEKEGLEGTITTKPLAPNPSFSPTPGFTPLGFSVPVPSSTFTSSSTYT 300
QY 291 SCDSNFGAVASPSETAPPHLKAGPIILPGPPASTHLCTPGPASTHLCTPGPASTHLCT 350
DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIIP 335
QY 351 TPVCKWESASAPADQADADPATIYAVVDGVPSPRKEVLVRIGLSHEIRLEENGR 410
DB 336 NPLQWEDSA-HKPOSJLTDPTLYAVVENVPPLRMEFVRRLGISHEDRLQLONGR 394
QY 411 HUREQVSMLAAMRRRTPRREATTLELGRVLRDMDLGLCLENIBERLGAARLASEPRL 470
DB 395 CLREQVSMLATWRRRTPRREATTLELGRVLRDMDLGLCLENIBERLGAARLASEPRL 454

```

RESULT 14

US-08-050-319B-25
Sequence 25, Application US/08050319B
Patent No. 5633145

GENERAL INFORMATION:

APPLICANT: M. Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFaIpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050.319B

FILING DATE: 10-May-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-050-319B-25

Query Match 58.1%; Score 1512; DB 1; Length 455;

Best Local Similarity 62.7%; Pred. No. 3,6e-111;

Matches 301; Conservative 38; Mismatches 105; Indels 36; Gaps 7;

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QY 1 MGLPTVPGILLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
DB 1 MGLSTVPDLILLPLVLELVGIYPSGVIGLVPHLADREKRDSDVCPQKXIHPONNISICT 60
QY 61 KCHKGTLYNDCPGRGDTDCRCVCAFGTYTALLENHRLCSGRCDMPFOVEISPCVVD 120
DB 61 KCHKGTLYNDCPGRGDTDCRCESGSGFTASENHLRCLSCSKRKMGOVEISSCTVD 120
QY 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCOERODTICHMGFFLGAKCI 180
DB 121 RDTVCGCRKNQYRHYMSENLFCQCFNCSLCLNGTVHLSQEKONTVCTCHAGFFLAENECV 180
QY 181 SCHDCKK-EECKLCPTPSTGKSDODPGTTLVLPVIVFGICLASFASVVLACYORWK 239
DB 181 SCNCKKSLBECTKCLPQIENVKGTEDSGTTLVLPVIFFGICLLSLFIFGLMYRYORWK 240
QY 240 PLYSIIIGQSTLVKEGPE-----LVPAFGFNP-----TTTICPSSTPSSSPVSIPIYI 290
DB 241 SKLVSIVCGKSTPEKEGLEGTITTKPLAPNPSFSPTPGFTPLGFSVPVPSSTFTSSSTYT 300
QY 291 SCDSNFGAVASPSETAPPHLKAGPIILPGPPASTHLCTPGPASTHLCTPGPASTHLCT 350
DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIIP 335
QY 351 TPVCKWESASAPADQADADPATIYAVVDGVPSPRKEVLVRIGLSHEIRLEENGR 410
DB 336 NPLQWEDSA-HKPOSJLTDPTLYAVVENVPPLRMEFVRRLGISHEDRLQLONGR 394
QY 411 HUREQVSMLAAMRRRTPRREATTLELGRVLRDMDLGLCLENIBERLGAARLASEPRL 470
DB 395 CLREQVSMLATWRRRTPRREATTLELGRVLRDMDLGLCLENIBERLGAARLASEPRL 454

```

RESULT 15

US-08-465-982-25
Sequence 25, Application US/08465982
Patent No. 5863786

GENERAL INFORMATION:

APPLICANT: M. Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFaIpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.982

FILING DATE: 10-May-1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/050.319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-982-25

Query Match 58.1%; Score 1512; DB 2; Length 455;
Best Local Similarity 62.7%; Pred. No. 3,66-111;

Matches 301; Conservative 36; Mismatches 105; Indels 36; Gaps 7;

```
QY 1 MGLEPTVPGILLPLVLPLADLVPAVGAVPHRGDLEKRESPPQGRKYNHPQNSTICCT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MGISTVPDLPLPLVLPLGLVPSGVIGLPHLDREKRDVCPQGRYIHPQNNISICT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 KCHKGTLYNDCCPGGRDTCRCVCAPGTYTALLENHRLRCLSCSRQDEMFQVEISPCVVD 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 KCHKGTLYNDCCPGGRDTCRCVCAPGTYTALLENHRLRCLSCSRQDEMFQVEISPCVVD 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 RDTVCGCRKQYRHYWGEYGFRCINCSICPENGTVNIPQGRQDTTICHQMGFFLKAKCI 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 RDTVCGCRKQYRHYWGEYGFRCINCSICPENGTVNIPQGRQDTTICHQMGFFLKAKCI 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 181 SCHDCKRK-EGEKLCPTRPSTGKXSDPGCTVLLPLVIVFGLCLASPASVYLACRYORMK 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 SCHDCKRK-EGEKLCPTRPSTGKXSDPGCTVLLPLVIVFGLCLASPASVYLACRYORMK 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 240 PKLYSIICGOSTLVKEGEPE-----LVPAPGPNP---TTICFSSSTPSSSPVSIPIYI 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 240 PKLYSIICGOSTLVKEGEPE-----LVPAPGPNP---TTICFSSSTPSSSPVSIPIYI 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 291 SCDSRNFGAVASPSSETPAPHLKAGPIILGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 291 SCDSRNFGAVASPSSETPAPHLKAGPIILGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDP1P 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDP1P 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 351 TPVQKMEASASAPDQADADPATLYAVVDGVPSPKELVRLGLSEHETIRLELENGR 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 351 TPVQKMEASASAPDQADADPATLYAVVDGVPSPKELVRLGLSEHETIRLELENGR 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 394 NPLQKWEUSA-HKQSLDTPDPTLYAVVENPPLRKKEFVRRLGSLSDHEIDRLQLONGR 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 394 NPLQKWEUSA-HKQSLDTPDPTLYAVVENPPLRKKEFVRRLGSLSDHEIDRLQLONGR 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 411 HLRBAQYSMLAAMRRRTPRRATLELLGRVLRMDMLGCLLENIEBALGAARLASERPRL 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 411 HLRBAQYSMLAAMRRRTPRRATLELLGRVLRMDMLGCLLENIEBALGAARLASERPRL 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 454 CLRBAQYCMLATWRRTPRRATLELLGRVLRMDMLGCLLENIEBALGPALPPAPSL 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 454 CLRBAQYCMLATWRRTPRRATLELLGRVLRMDMLGCLLENIEBALGPALPPAPSL 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: September 13, 2003, 07:06:40
Job time : 23 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:05:40 ; Search time 26 Seconds

(without alignments)
2643.260 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603 1 MGLPTVPGALLPLVLPALLA.....NIEBALGGAARLASEPRILW 471

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2603	100.0	471	9	US-09-970-532-2
2	1519	58.4	455	15	US-10-252-408-4
3	1517	58.3	455	9	US-09-826-212-3
4	1517	58.3	455	9	US-09-333-966-5
5	1517	58.3	455	9	US-09-027-287-3
6	1517	58.3	455	9	US-09-874-138-3
7	1517	58.3	455	9	US-09-840-707A-16
8	1517	58.3	455	9	US-09-252-656B-3
9	1517	58.3	455	9	US-09-899-422-2
10	1517	58.3	455	10	US-09-899-422-17
11	1517	58.3	455	10	US-09-935-727-5
12	1517	58.3	455	10	US-09-898-234-2
13	1517	58.3	455	10	US-09-898-234-17
14	1517	58.3	455	10	US-09-756-854-5
15	1517	58.3	455	10	US-09-899-429A-2

16	1517	58.3	455	10	US-09-899-429A-27	Sequence 27, Appli
17	1517	58.3	455	10	US-09-792-356-2	Sequence 2, Appli
18	1517	58.3	455	10	US-09-792-356-17	Sequence 17, Appli
19	1517	58.3	455	11	US-09-314-889-5	Sequence 5, Appli
20	1517	58.3	455	13	US-10-005-842-3	Sequence 3, Appli
21	1517	58.3	455	14	US-10-120-397-2	Sequence 2, Appli
22	1517	58.3	455	15	US-10-041-574-5	Sequence 5, Appli
23	1517	58.3	455	14	US-10-038-557A-16	Sequence 16, Appli
24	1517	58.3	455	15	US-10-175-902-4	Sequence 4, Appli
25	1517	58.3	455	15	US-10-186-643-3	Sequence 3, Appli
26	1511	58.0	455	15	US-09-945-505-3	Sequence 3, Appli
27	1500.5	57.6	909	15	US-10-226-296-4	Sequence 4, Appli
28	1500.5	57.6	909	15	US-10-226-318-4	Sequence 4, Appli
29	1325.5	50.9	461	9	US-09-899-422-15	Sequence 15, Appli
30	1325.5	50.9	461	10	US-09-898-234-15	Sequence 15, Appli
31	1325.5	50.9	461	10	US-09-899-429A-25	Sequence 25, Appli
32	1325.5	50.9	461	10	US-09-792-356-15	Sequence 15, Appli
33	1178	45.3	371	9	US-09-899-422-12	Sequence 12, Appli
34	1178	45.3	371	10	US-09-898-234-12	Sequence 12, Appli
35	1178	45.3	371	10	US-09-792-356-12	Sequence 12, Appli
36	1171	45.0	371	10	US-09-899-429A-22	Sequence 22, Appli
37	1072	41.2	181	9	US-09-970-532-4	Sequence 4, Appli
38	874	33.6	247	15	US-10-193-616-10	Sequence 10, Appli
39	834.5	32.1	213	14	US-10-125-062-1	Sequence 1, Appli
40	832.5	32.0	211	10	US-09-899-429A-8	Sequence 8, Appli
41	813.5	31.3	197	14	US-10-112-793-21	Sequence 21, Appli
42	813.5	31.3	201	10	US-09-899-429A-14	Sequence 14, Appli
43	772	29.7	200	10	US-09-899-429A-12	Sequence 12, Appli
44	753	28.9	190	10	US-09-899-429A-18	Sequence 18, Appli
45	738.5	28.4	183	10	US-09-899-429A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-970-532-2
Sequence 2, Application US/09970532
Patent No. US2002007675A1
GENERAL INFORMATION:
APPLICANT: Taylor, J. Michael
APPLICANT: Kenrill, J.F., Marcus
APPLICANT: Lee, Eun-Kyung
TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 06411-018001
CURRENT FILING DATE: 2001-10-03
PRIORITY FILING DATE: 09/513,007
PRIOR APPLICATION NUMBER: 2000-02-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 471
TYPE: PRT
ORGANISM: Bos taurus
US-09-970-532-2

Query Match 100.0%; Score 2603; DB 9; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGLPTVPGALLPLVLPALLADYVAGVGVLPHPGDLKRESPOCGKYNPNSTICT	60
DB	1	MGLPTVPGALLPLVLPALLADYVAGVGVLPHPGDLKRESPOCGKYNPNSTICT	60
QY	61	KCHGTYLYNDPCPGGRDTCVCAPGTYTALBNHLRCLSCSRCDMPVBSIPCVVD	120
DB	61	KCHGTYLYNDPCPGGRDTCVCAPGTYTALBNHLRCLSCSRCDMPVBSIPCVVD	120
QY	121	RDYCGCKRNOYREYWGRTGRCLNCSICPGTYTNIPOEQRDPTICGCHKMGPFLKAGNCI	180
DB	121	RDYCGCKRNOYREYWGRTGRCLNCSICPGTYTNIPOEQRDPTICGCHKMGPFLKAGNCI	180

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Db      121 RDTVCGCRKNQRYREWGTFGRCLNCSLCPNGVTNIPQERODTICHCHMGFLKAGACT 180
Qy      121 SCHDCKNCECEKLCPRPSTGKDSODPGTTLPLVTVFGLCLASASVYLACRQWRMP 240
Db      121 SCHDCKNCECEKLCPRPSTGKDSODPGTTLPLVTVFGLCLASASVYLACRQWRMP 240
Qy      241 KLYSIICGOSTLVKGEPELVLVAPGFNFTTICSSSTPSSSPVSIPIYISCDRSNFGAV 300
Db      241 KLYSIICGOSTLVKGEPELVLVAPGFNFTTICSSSTPSSSPVSIPIYISCDRSNFGAV 300
Qy      301 ASPSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPGVQKWEASA 360
Db      301 ASPSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPGVQKWEASA 360
Qy      361 PSAPQLADADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGRHIREAQYSML 420
Db      361 PSAPQLADADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGRHIREAQYSML 420
Qy      421 AAMRRRTPRREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 471
Db      421 AAMRRRTPRREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 471

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RESULT 2

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US-10-252-408-4
/ Sequence 4, Application US/10252408
/ Publication No. US20030082736A1
/ GENERAL INFORMATION:
/ APPLICANT: SMITH, Craig A.
/ TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
/ FILE REFERENCE: A-71592
/ CURRENT APPLICATION NUMBER: US/10/252,408
/ PRIOR FILING DATE: 2002-09-24
/ PRIOR APPLICATION NUMBER: US/08/406,824
/ PRIOR FILING DATE: 1995-03-20
/ PRIOR APPLICATION NUMBER: US 08/255,849
/ PRIOR FILING DATE: 1994-06-08
/ PRIOR APPLICATION NUMBER: US 07/860,710
/ PRIOR FILING DATE: 1992-03-30
/ PRIOR APPLICATION NUMBER: US 07/523,635
/ PRIOR FILING DATE: 1990-05-10
/ PRIOR APPLICATION NUMBER: US 07/421,417
/ PRIOR FILING DATE: 1989-10-13
/ PRIOR APPLICATION NUMBER: US 07/405,370
/ PRIOR FILING DATE: 1989-09-11
/ PRIOR APPLICATION NUMBER: US 07/403,241
/ PRIOR FILING DATE: 1989-09-05
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 4
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-252-408-4

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Query Match      58.4%; Score 1519; DB 15; Length 455;
Best Local Similarity 62.9%; Pred. No. 5,1e-101;
Matches 302; Conservative 39; Mismatches 103; Indels 36; Gaps 7;

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Qy      1 MGLPTVPGILLPLVLPALLADVPAGVQGLVPHPDLEKRESPPCQKKNHPONSTICT 60
Db      1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLDREKRDSVCPQKVIHPONNSICT 60
Qy      61 KCHKGTLYINDCPGGRDTCRCVCAFGTYTALLENHLRCLSCSRCDMPQVEISPCYVD 120
Db      61 KCHKGTLYINDCPGGRDTCRCVCAFGTYTALLENHLRCLSCSRCDMPQVEISPCYVD 120
Qy      121 RDTVCGCRKNQRYREWGTFGRCLNCSLCPNGVTNIPQERODTICHCHMGFLKAGACT 180
Db      121 RDTVCGCRKNQRYREWGTFGRCLNCSLCPNGVTNIPQERODTICHCHMGFLKAGACT 180
Qy      181 SCHDCKN-EEBKLCPTPRSTGKDSODPGTTLPLVTVFGLCLASASVYLACRQWRMP 239
Db      181 SCHDCKN-EEBKLCPTPRSTGKDSODPGTTLPLVTVFGLCLASASVYLACRQWRMP 239

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Db      181 SCNNCKSLBECTKLCPLQIENVKGTEDSGTTLPLVTVFGLCLSLFLIGLSYRQWRK 240
Qy      240 PKLYSIICGOSTLVKGEPELVLVAPGFNFTTICSSSTPSSSPVSIPIYI 290
Db      241 SKLYSIICGOSTLVKGEPELVLVAPGFNFTTICSSSTPSSSPVSIPIYI 290
Qy      291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGVQKWEASA 350
Db      291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGVQKWEASA 350
Qy      351 TPVQKWEASAPADPADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGRHIREAQYSML 410
Db      351 TPVQKWEASAPADPADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGRHIREAQYSML 410
Qy      411 HIREAQYSMLAAMRRRTPRREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 470
Db      411 HIREAQYSMLAAMRRRTPRREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 470
Qy      470 HIREAQYSMLAAMRRRTPRREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 470
Db      470 HIREAQYSMLAAMRRRTPRREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 470

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RESULT 3

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US-09-826-212-3
/ Sequence 3, Application US/09826212
/ Patent No. US20010021516A1
/ GENERAL INFORMATION:
/ APPLICANT: Wei, Ying-Fei
/ APPLICANT: Ruben, Steven
/ APPLICANT: Gentz, Reinex
/ APPLICANT: Ni, Jian
/ TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
/ FILE REFERENCE: 1488,128006
/ CURRENT APPLICATION NUMBER: US/09/826,212
/ PRIOR FILING DATE: 2001-04-05
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: Patent version 3.0
/ SEQ ID NO 3
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-826-212-3

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Query Match      58.3%; Score 1517; DB 9; Length 455;
Best Local Similarity 62.9%; Pred. No. 7,1e-101;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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Qy      1 MGLPTVPGILLPLVLPALLADVPAGVQGLVPHPDLEKRESPPCQKKNHPONSTICT 60
Db      1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLDREKRDSVCPQKVIHPONNSICT 60
Qy      61 KCHKGTLYINDCPGGRDTCRCVCAFGTYTALLENHLRCLSCSRCDMPQVEISPCYVD 120
Db      61 KCHKGTLYINDCPGGRDTCRCVCAFGTYTALLENHLRCLSCSRCDMPQVEISPCYVD 120
Qy      121 RDTVCGCRKNQRYREWGTFGRCLNCSLCPNGVTNIPQERODTICHCHMGFLKAGACT 180
Db      121 RDTVCGCRKNQRYREWGTFGRCLNCSLCPNGVTNIPQERODTICHCHMGFLKAGACT 180
Qy      181 SCHDCKN-EEBKLCPTPRSTGKDSODPGTTLPLVTVFGLCLASASVYLACRQWRMP 239
Db      181 SCHDCKN-EEBKLCPTPRSTGKDSODPGTTLPLVTVFGLCLASASVYLACRQWRMP 239
Qy      239 SCHDCKN-EEBKLCPTPRSTGKDSODPGTTLPLVTVFGLCLASASVYLACRQWRMP 239
Db      239 SCHDCKN-EEBKLCPTPRSTGKDSODPGTTLPLVTVFGLCLASASVYLACRQWRMP 239
Qy      240 PKLYSIICGOSTLVKGEPELVLVAPGFNFTTICSSSTPSSSPVSIPIYI 290
Db      240 PKLYSIICGOSTLVKGEPELVLVAPGFNFTTICSSSTPSSSPVSIPIYI 290
Qy      291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGVQKWEASA 350
Db      291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGVQKWEASA 350
Qy      351 TPVQKWEASAPADPADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGRHIREAQYSML 410
Db      351 TPVQKWEASAPADPADPATLYAVVDGVPSPRWKELVRLGLSEHEIERLEENGRHIREAQYSML 410
Qy      411 HIREAQYSMLAAMRRRTPRREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 470
Db      411 HIREAQYSMLAAMRRRTPRREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 470

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Db 395 CLREAQYSLMAYRRRTFRREATTLELLGRVLRMDMLGCLDIEDBALCGPALPPAPSL 454

RESULT 4

US-09-333-966-5

Sequence 5, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333, 966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815, 469
FILING DATE:
APPLICATION NUMBER: NO. US20020009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028, 711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013, 285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36, 688
REFERENCE/DOCKET NUMBER: 1488, 0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
STRANDNESS: NO. US20020009773A1 Relevantant
TOPOLOGY: NO. US20020009773A1 Relevantant
MOLECULE TYPE: protein
US-09-333-966-5

Query Match 58.3%; Score 1517; DB 9; Length 455;
Best Local Similarity 62.9%; Pred. No. 7.1e-101;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGLLPLVLPALLADYVAGVQGLVPHPDLEKRESPPCGQKYNHPONSTICT 60
DB 1 MGLSTVPGLLPLVLELAVGIVPSGVGLVPHLDREKRSVCPQKTIHPONNSICT 60
QY 61 KCHGTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDREMFVLEISPCYVD 120
DB 61 KCHGTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDREMFVLEISPCYVD 120
QY 61 KCHGTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDREMFVLEISPCYVD 120
DB 61 KCHGTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDREMFVLEISPCYVD 120
QY 121 RDTYCGCKNOYREWGRTGRCLNCSLCFPGTNNI PCOERODTICHGMGFFLGACI 180
DB 121 RDTYCGCKNOYREWGRTGRCLNCSLCFPGTNNI PCOERODTICHGMGFFLGACI 180

Db 121 RDTYCGCKNOYRYWSENLFQCFNCSLCNGTVHLSQCEKONTVCTCHAGFLRENECV 180
QY 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASFVAVLACRYORWK 239
Db 181 SCNCKKSLECTKLCPLQENVKGTBDGTTVLPLVIFGLCLSLFLFGLMRYORWK 240
QY 240 PKLYSIICGSTLYKEGPE-----LVVAPGNP-----TTTICRSSTPSSPVSIPIYI 290
Db 241 SKLYSIYCGKSTPEKEGELTGTTRKPLAFNPSFSPFTPLTGFSPVPSSTFTSSSTYT 300
QY 291 SCDSNFGAVASPESEAPPHLKAGPLIGPPASTHLCCTPPASTHLCCTGPPASTHLC 350
Db 301 FGDGPNF---AAPREVAAPYQADPIL-----ATAL-----ASDPI 335
QY 351 TPVCKEASAPADOLADADPATLYAVVGVPPSRWELVRRLGSLSEHIELENGR 410
Db 336 NPLQWESA-HKQSLDTDDPATLVAVVEVPLRWEPVRLGSLSEHIELENGR 394
QY 411 HLEDAQYSLMAYRRRTFRREATTLELLGRVLRMDMLGCLDIEDBALCGPALPPAPSL 470
Db 395 CLREAQYSLMAYRRRTFRREATTLELLGRVLRMDMLGCLDIEDBALCGPALPPAPSL 454

RESULT 5

US-09-027-287-3

Sequence 3, Application US/09027287A
Patent No. US20020064869A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ullrich, Stephen
TITLE OF INVENTION: Apoptosis Inducing Molecule II
FILE REFERENCE: 1488, 0650004
CURRENT APPLICATION NUMBER: US/09/027, 287A
FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 09/003, 886
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 08/822, 953
EARLIER FILING DATE: 1997-03-21
EARLIER APPLICATION NUMBER: US 60/030, 157
EARLIER FILING DATE: 1996-10-31
EARLIER APPLICATION NUMBER: US 60/013, 923
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-027-287-3

Query Match 58.3%; Score 1517; DB 9; Length 455;
Best Local Similarity 62.9%; Pred. No. 7.1e-101;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGLLPLVLPALLADYVAGVQGLVPHPDLEKRESPPCGQKYNHPONSTICT 60
Db 1 MGLSTVPGLLPLVLELAVGIVPSGVGLVPHLDREKRSVCPQKTIHPONNSICT 60
QY 61 KCHGTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDREMFVLEISPCYVD 120
Db 61 KCHGTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDREMFVLEISPCYVD 120
QY 121 RDTYCGCKNOYREWGRTGRCLNCSLCFPGTNNI PCOERODTICHGMGFFLGACI 180
Db 121 RDTYCGCKNOYRYWSENLFQCFNCSLCNGTVHLSQCEKONTVCTCHAGFLRENECV 180
QY 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASFVAVLACRYORWK 239
Db 181 SCNCKKSLECTKLCPLQENVKGTBDGTTVLPLVIFGLCLSLFLFGLMRYORWK 240
QY 240 PKLYSIICGSTLYKEGPE-----LVVAPGNP-----TTTICRSSTPSSPVSIPIYI 290
Db 240 PKLYSIICGSTLYKEGPE-----LVVAPGNP-----TTTICRSSTPSSPVSIPIYI 290

Db 241 SKLVSIVCGKSTPEKEGELBEGTTTKPLAHPSPFSTPGFTTLGSPVPSSTFTSSSTYT 300
Qy 291 SCDSNFGAVASPSSETAPPHLKAGPILGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
Db 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVOKMEASAPAPQADADPATLYAVVDGVPSPRWKELVRRLGLSHEIERLENGR 410
Db 336 NPLQKMEBSA-HKPSLTDDBPATLYAVVENVPPLRMKEFVRRLGLSDHEIDRLQNGR 394
Qy 411 HUREAQSMLAAMRRRTREARETLELGRVLRDMDLGLCLENIEBALGGAARLASERPIL 470
Db 395 CLREAQYSMLATWRRRTREARETLELGRVLRDMDLGLCLEDIEBALGPAALPPAPSL 454

RESULT 6
US-09-874-138-3

/ Sequence 3, Application US/09874138
/ Patent No. US20020072091A1
/ GENERAL INFORMATION:
/ APPLICANT: N.Y. Jiar
/ APPLICANT: Genetz, Reiner L.
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Rosen, Craig A.
/ TITLE OF INVENTION: Death Domain Containing Receptor 5
/ FILE REFERENCE: 1488.1310006
/ CURRENT APPLICATION NUMBER: US/09/874.138
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 09/565.009
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: 60/148.939
/ PRIOR FILING DATE: 1999-08-13
/ PRIOR APPLICATION NUMBER: 60/133.238
/ PRIOR FILING DATE: 1999-05-07
/ PRIOR APPLICATION NUMBER: 60/132.498
/ PRIOR FILING DATE: 1999-05-04
/ PRIOR APPLICATION NUMBER: 09/042.583
/ PRIOR FILING DATE: 1998-03-17
/ PRIOR APPLICATION NUMBER: 60/054.021
/ PRIOR FILING DATE: 1997-07-29
/ PRIOR APPLICATION NUMBER: 60/040.846
/ PRIOR FILING DATE: 1997-03-17
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-874-138-3

Query Match 58.3%; Score 1517; DB 9; Length 455;
Best Local Similarity 62.9%; Pred. No. 7.1e-101;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGLLPLVLPALLADVPAGVQGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
Db 1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLDREKRDVSCGKVIHPONNSICT 60
Qy 61 KCHKTYIYNDGPGGRDTCRVCAPGTYTALLENHRLCLSCSRGRDMPQVEISPCVVD 120
Db 61 KCHKTYIYNDGPGGRDTCRVCAPGTYTALLENHRLCLSCSRGRDMPQVEISPCVVD 120
Qy 121 RDTVCGCRKNQYREYMGRTGFRCLNCSLCPNGTVINPCOERODTICHGMGFLKAGCI 180
Db 121 RDTVCGCRKNQYREYMGRTGFRCLNCSLCPNGTVINPCOERODTICHGMGFLKAGCI 180
Qy 121 RDTVCGCRKNQYREYMGRTGFRCLNCSLCPNGTVINPCOERODTICHGMGFLKAGCI 180
Db 121 RDTVCGCRKNQYREYMGRTGFRCLNCSLCPNGTVINPCOERODTICHGMGFLKAGCI 180
Qy 181 SCHDCRKN-ECEKLCPTRPSTGKDSQDPGTVLLPLVIVFGICLASFASVVLACRYQRMK 239
Db 181 SCHDCRKN-ECEKLCPTRPSTGKDSQDPGTVLLPLVIVFGICLASFASVVLACRYQRMK 239
Qy 181 SCNSCKSLEKCTKCLPQIEHVKGTEBGGTVLLPLVIFGICLSLFLIGLMRYQRMK 240
Db 181 SCNSCKSLEKCTKCLPQIEHVKGTEBGGTVLLPLVIFGICLSLFLIGLMRYQRMK 240
Qy 240 PKLVSIIIGOSTLVKGEPE-----LVVAPAGNP-----TTTICSSSTPSSSPVSIPIYI 290
Db 240 PKLVSIIIGOSTLVKGEPE-----LVVAPAGNP-----TTTICSSSTPSSSPVSIPIYI 290

Db 241 SKLVSIVCGKSTPEKEGELBEGTTTKPLAHPSPFSTPGFTTLGSPVPSSTFTSSSTYT 300
Qy 291 SCDSNFGAVASPSSETAPPHLKAGPILGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
Db 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVOKMEASAPAPQADADPATLYAVVDGVPSPRWKELVRRLGLSHEIERLENGR 410
Db 336 NPLQKMEBSA-HKPSLTDDBPATLYAVVENVPPLRMKEFVRRLGLSDHEIDRLQNGR 394
Qy 411 HUREAQSMLAAMRRRTREARETLELGRVLRDMDLGLCLENIEBALGGAARLASERPIL 470
Db 395 CLREAQYSMLATWRRRTREARETLELGRVLRDMDLGLCLEDIEBALGPAALPPAPSL 454

RESULT 7
US-09-840-707A-16

/ Sequence 16, Application US/09840707A
/ Patent No. US2002007276A1
/ GENERAL INFORMATION:
/ APPLICANT: Fredeking, Terry M.
/ APPLICANT: Ignatyev, George M.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
/ FILE REFERENCE: 2481-301C
/ CURRENT APPLICATION NUMBER: US/09/840.707A
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: 09/562.979
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: 60/198.210
/ PRIOR FILING DATE: 1999-04-27
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 16
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Tumor Necrosis Factor p55 Receptor
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: AAA36753/GenBank
/ DATABASE ENTRY DATE: 1995-08-03
US-09-840-707A-16

Query Match 58.3%; Score 1517; DB 9; Length 455;
Best Local Similarity 62.9%; Pred. No. 7.1e-101;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGLLPLVLPALLADVPAGVQGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
Db 1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLDREKRDVSCGKVIHPONNSICT 60
Qy 61 KCHKTYIYNDGPGGRDTCRVCAPGTYTALLENHRLCLSCSRGRDMPQVEISPCVVD 120
Db 61 KCHKTYIYNDGPGGRDTCRVCAPGTYTALLENHRLCLSCSRGRDMPQVEISPCVVD 120
Qy 121 RDTVCGCRKNQYREYMGRTGFRCLNCSLCPNGTVINPCOERODTICHGMGFLKAGCI 180
Db 121 RDTVCGCRKNQYREYMGRTGFRCLNCSLCPNGTVINPCOERODTICHGMGFLKAGCI 180
Qy 121 RDTVCGCRKNQYREYMGRTGFRCLNCSLCPNGTVINPCOERODTICHGMGFLKAGCI 180
Db 121 RDTVCGCRKNQYREYMGRTGFRCLNCSLCPNGTVINPCOERODTICHGMGFLKAGCI 180
Qy 181 SCHDCRKN-ECEKLCPTRPSTGKDSQDPGTVLLPLVIVFGICLASFASVVLACRYQRMK 239
Db 181 SCHDCRKN-ECEKLCPTRPSTGKDSQDPGTVLLPLVIVFGICLASFASVVLACRYQRMK 239
Qy 181 SCNSCKSLEKCTKCLPQIEHVKGTEBGGTVLLPLVIFGICLSLFLIGLMRYQRMK 240
Db 181 SCNSCKSLEKCTKCLPQIEHVKGTEBGGTVLLPLVIFGICLSLFLIGLMRYQRMK 240
Qy 240 PKLVSIIIGOSTLVKGEPE-----LVVAPAGNP-----TTTICSSSTPSSSPVSIPIYI 290
Db 240 PKLVSIIIGOSTLVKGEPE-----LVVAPAGNP-----TTTICSSSTPSSSPVSIPIYI 290
Qy 291 SCDSNFGAVASPSSETAPPHLKAGPILGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
Db 291 SCDSNFGAVASPSSETAPPHLKAGPILGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
Qy 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
Db 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVOKMEASAPAPQADADPATLYAVVDGVPSPRWKELVRRLGLSHEIERLENGR 410
Db 351 TPVOKMEASAPAPQADADPATLYAVVDGVPSPRWKELVRRLGLSHEIERLENGR 410

Db 336 NPLQKWEBSA-HKQSLDTPDPAVLAVENVPPLRKKEFVRRLGLSDHEIDRLQNGR 394
 Oy 411 HLEAQSMLAAMRRTPREATLELGRVLRDMDLGCLENIEEALGAARLASERPL 470
 Db 395 CLREAQYSMLATWRRTTPREATLELGRVLRDMDLGCLEDIEBALCGPALPPASPL 454

RESULT 8

US-09-252-656B-3
 : Sequence 3, Application US/092525656B
 : Patent No. US20020081647A1
 : GENERAL INFORMATION:
 : APPLICANT: Ebner, Reinhard
 : APPLICANT: Yu, Guo-Liang
 : APPLICANT: Ruben, Steven M.
 : APPLICANT: Zhang, Jun
 : APPLICANT: Ullrich, Stephen
 : APPLICANT: Zhai, Yifan
 : TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
 : FILE REFERENCE: 1488,065006
 : CURRENT APPLICATION NUMBER: US/09/252,656B
 : PRIOR FILING DATE: 1999-02-19
 : PRIOR APPLICATION NUMBER: US 60/075,409
 : PRIOR FILING DATE: 1998-02-20
 : PRIOR APPLICATION NUMBER: US 09/027,287
 : PRIOR FILING DATE: 1998-02-20
 : PRIOR APPLICATION NUMBER: US 09/003,886
 : PRIOR FILING DATE: 1998-01-07
 : PRIOR APPLICATION NUMBER: US 08/822,953
 : PRIOR FILING DATE: 1997-03-21
 : PRIOR APPLICATION NUMBER: US 60/013,923
 : PRIOR FILING DATE: 1996-03-22
 : PRIOR APPLICATION NUMBER: US 60/030,157
 : PRIOR FILING DATE: 1996-10-31
 : NUMBER OF SEQ ID NOS: 61
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 3
 : LENGTH: 455
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-252-656B-3

Query Match 58.3%; Score 1517; DB 9; Length 455;
 Best Local Similarity 62.9%; Pred. No. 7,1e-101;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Oy 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHRDLERKESPCQGRKYNHPONSTICT 60
 Db 1 MGLSTVPDLLPLVLLLELVGIVPSGVIGLVPHLGDREKRDVSCQGXIHPONNISICT 60
 Oy 61 KCHGTYLYNDCCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRDMPFVEISPCVVD 120
 Db 61 KCHKTYLYNDCCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRDMPFVEISPCVVD 120
 Oy 121 RDTVCGCKNORYREXWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMFFLGAKCI 180
 Db 121 RDTVCGCKNORYREXWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMFFLGAKCI 180
 Oy 121 RDTVCGCKNORYREXWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMFFLGAKCI 180
 Db 121 RDTVCGCKNORYREXWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMFFLGAKCI 180
 Oy 181 SCHDCKN-EECKLCPTRPSTGKSODPGTTLPLVIVFGICLASFASVYLACYGRWK 239
 Db 181 SCHDCKN-EECKLCPTRPSTGKSODPGTTLPLVIVFGICLASFASVYLACYGRWK 239
 Oy 181 SCHDCKN-EECKLCPTRPSTGKSODPGTTLPLVIVFGICLASFASVYLACYGRWK 239
 Db 181 SCHDCKN-EECKLCPTRPSTGKSODPGTTLPLVIVFGICLASFASVYLACYGRWK 239
 Oy 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSPTSSSPVSIPIYI 290
 Db 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSPTSSSPVSIPIYI 290
 Oy 241 SKLYSIIVGKSTPEKEGLEGTITTKPLAPNPSFSPTPGFTPLGSSPVSSSTFTSSSTYT 300
 Db 241 SKLYSIIVGKSTPEKEGLEGTITTKPLAPNPSFSPTPGFTPLGSSPVSSSTFTSSSTYT 300
 Oy 291 SCDSNFGAVASPSETAPPHLKAGPILEGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 Db 291 SCDSNFGAVASPSETAPPHLKAGPILEGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 Oy 301 PGDCNPF---AAPREVAPPYOGADPIL-----ATAL-----ASDPFP 335
 Db 301 PGDCNPF---AAPREVAPPYOGADPIL-----ATAL-----ASDPFP 335
 Oy 351 TPVQKWEASAPADPADADPATLYAVVDVPSRKELVRLGLSHEIERLENGR 410
 Db 351 TPVQKWEASAPADPADADPATLYAVVDVPSRKELVRLGLSHEIERLENGR 410

Db 336 NPLQKWEBSA-HKQSLDTPDPAVLAVENVPPLRKKEFVRRLGLSDHEIDRLQNGR 394
 Oy 411 HLEAQSMLAAMRRTPREATLELGRVLRDMDLGCLENIEEALGAARLASERPL 470
 Db 395 CLREAQYSMLATWRRTTPREATLELGRVLRDMDLGCLEDIEBALCGPALPPASPL 454

RESULT 9

US-09-899-422-2
 : Sequence 2, Application US/09899422
 : Patent No. US20020090676A1
 : GENERAL INFORMATION:
 : APPLICANT: Hauptmann, Rudolph
 : APPLICANT: Hamlet, Adolph
 : APPLICANT: Maurer-Fogy, Ingrid
 : APPLICANT: Stralowa, Christian
 : TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
 : TITLE OF INVENTION: Then
 : FILE REFERENCE: 98,385-H
 : CURRENT APPLICATION NUMBER: US/09/899,422
 : PRIOR FILING DATE: 2001-08-21
 : PRIOR APPLICATION NUMBER: 09/525,998
 : PRIOR FILING DATE: 2000-03-15
 : PRIOR APPLICATION NUMBER: 08/383,676
 : PRIOR FILING DATE: 1995-02-01
 : PRIOR APPLICATION NUMBER: 08/153,287
 : PRIOR FILING DATE: 1993-11-17
 : PRIOR APPLICATION NUMBER: 07/821,750
 : PRIOR FILING DATE: 1992-01-02
 : PRIOR APPLICATION NUMBER: 07/511,430
 : PRIOR FILING DATE: 1990-04-20
 : NUMBER OF SEQ ID NOS: 87
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 2
 : LENGTH: 455
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-899-422-2

Query Match 58.3%; Score 1517; DB 9; Length 455;
 Best Local Similarity 62.9%; Pred. No. 7,1e-101;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Oy 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHRDLERKESPCQGRKYNHPONSTICT 60
 Db 1 MGLSTVPDLLPLVLLLELVGIVPSGVIGLVPHLGDREKRDVSCQGXIHPONNISICT 60
 Oy 61 KCHGTYLYNDCCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRDMPFVEISPCVVD 120
 Db 61 KCHKTYLYNDCCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRDMPFVEISPCVVD 120
 Oy 121 RDTVCGCKNORYREXWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMFFLGAKCI 180
 Db 121 RDTVCGCKNORYREXWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMFFLGAKCI 180
 Oy 121 RDTVCGCKNORYREXWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMFFLGAKCI 180
 Db 121 RDTVCGCKNORYREXWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMFFLGAKCI 180
 Oy 181 SCHDCKN-EECKLCPTRPSTGKSODPGTTLPLVIVFGICLASFASVYLACYGRWK 239
 Db 181 SCHDCKN-EECKLCPTRPSTGKSODPGTTLPLVIVFGICLASFASVYLACYGRWK 239
 Oy 181 SCHDCKN-EECKLCPTRPSTGKSODPGTTLPLVIVFGICLASFASVYLACYGRWK 239
 Db 181 SCHDCKN-EECKLCPTRPSTGKSODPGTTLPLVIVFGICLASFASVYLACYGRWK 239
 Oy 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSPTSSSPVSIPIYI 290
 Db 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSPTSSSPVSIPIYI 290
 Oy 241 SKLYSIIVGKSTPEKEGLEGTITTKPLAPNPSFSPTPGFTPLGSSPVSSSTFTSSSTYT 300
 Db 241 SKLYSIIVGKSTPEKEGLEGTITTKPLAPNPSFSPTPGFTPLGSSPVSSSTFTSSSTYT 300
 Oy 291 SCDSNFGAVASPSETAPPHLKAGPILEGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 Db 291 SCDSNFGAVASPSETAPPHLKAGPILEGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 Oy 301 PGDCNPF---AAPREVAPPYOGADPIL-----ATAL-----ASDPFP 335
 Db 301 PGDCNPF---AAPREVAPPYOGADPIL-----ATAL-----ASDPFP 335
 Oy 351 TPVQKWEASAPADPADADPATLYAVVDVPSRKELVRLGLSHEIERLENGR 410
 Db 351 TPVQKWEASAPADPADADPATLYAVVDVPSRKELVRLGLSHEIERLENGR 410
 Oy 411 HLEAQSMLAAMRRTPREATLELGRVLRDMDLGCLENIEEALGAARLASERPL 470
 Db 411 HLEAQSMLAAMRRTPREATLELGRVLRDMDLGCLENIEEALGAARLASERPL 470

Db 395 CLREAGYSLATWRRTTREATTELLGRLVLRMDMLGCLIEDIEALCGPALPAPASLL 454

RESULT 10

US-09-899-422-17
 ; Sequence 17, Application US/09899422
 ; Patent No. US20020090676A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hauptmann, Rudolph
 ; APPLICANT: Hummer, Adolph
 ; APPLICANT: Meurer-Fogel, Ingrid
 ; APPLICANT: Stralow, Christian
 ; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNA Coding for
 ; FILE REFERENCE: 98,385-H
 ; CURRENT APPLICATION NUMBER: US/09/899,422
 ; PRIOR FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: 09/525,998
 ; PRIOR FILING DATE: 2000-03-15
 ; PRIOR APPLICATION NUMBER: 08/383,676
 ; PRIOR FILING DATE: 1995-02-01
 ; PRIOR APPLICATION NUMBER: 08/153,287
 ; PRIOR FILING DATE: 1993-11-17
 ; PRIOR APPLICATION NUMBER: 07/821,750
 ; PRIOR FILING DATE: 1992-01-02
 ; PRIOR APPLICATION NUMBER: 07/511,430
 ; PRIOR FILING DATE: 1990-04-20
 ; NUMBER OF SEQ ID NOS: 87
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 455
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
 ; US-09-899-422-17

Query Match 58.3%; Score 1517; DB 9; Length 455;

Best Local Similarity 62.9%; Pred. No. 7,1e-101; Mismatches 104; Indels 36; Gaps 7;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGILLPLVLPALADVYAGVGVPHPDLEKESPCPOGKYNHPONSTICT 60
 DB 1 MGLSTVPLDLLPLVLELVIGYPSGVIGLVPHLDREKRDVSCQGXIHPONSICT 60
 QY 61 KCHKGTLYNDGPGGDDTCRCESGSGFTASENHLRCLSCSKRKGQVEISSCTVD 120
 DB 61 KCHKGTLYNDGPGGDDTCRCESGSGFTASENHLRCLSCSKRKGQVEISSCTVD 120
 QY 121 RDTVCGCRKQYREYWGEGTGRCLNCSLCPNGTINIICOERODTICHGMGFLKAGACI 180
 DB 121 RDTVCGCRKQYREYWGEGTGRCLNCSLCPNGTINIICOERODTICHGMGFLKAGACI 180
 QY 121 RDTVCGCRKQYREYWGEGTGRCLNCSLCPNGTINIICOERODTICHGMGFLKAGACI 180
 DB 121 RDTVCGCRKQYREYWGEGTGRCLNCSLCPNGTINIICOERODTICHGMGFLKAGACI 180
 QY 181 SCHDCRNR-ECKELCPTRPSTGKSDOPGTTVLLPLVIVGCLASFAVYLACRYGRWK 239
 DB 181 SCHDCRNR-ECKELCPTRPSTGKSDOPGTTVLLPLVIVGCLASFAVYLACRYGRWK 239
 QY 181 SCHDCRNR-ECKELCPTRPSTGKSDOPGTTVLLPLVIVGCLASFAVYLACRYGRWK 239
 DB 181 SCHDCRNR-ECKELCPTRPSTGKSDOPGTTVLLPLVIVGCLASFAVYLACRYGRWK 239
 QY 240 PKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICSSSTPSSPVSIPT 290
 DB 240 PKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICSSSTPSSPVSIPT 290
 QY 241 SKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICSSSTPSSPVSIPT 300
 DB 241 SKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICSSSTPSSPVSIPT 300
 QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
 DB 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
 QY 301 PGDCPNF---AARREVAAPYOGADPIL-----ATL-----ASDPI 335
 DB 301 PGDCPNF---AARREVAAPYOGADPIL-----ATL-----ASDPI 335
 QY 351 TPVQWEASAPADQADADPATLYAVVDGVPSSRWKELVRRIGLSEHEIERLENGR 410
 DB 351 TPVQWEASAPADQADADPATLYAVVDGVPSSRWKELVRRIGLSEHEIERLENGR 410
 QY 351 TPVQWEASAPADQADADPATLYAVVDGVPSSRWKELVRRIGLSEHEIERLENGR 410
 DB 351 TPVQWEASAPADQADADPATLYAVVDGVPSSRWKELVRRIGLSEHEIERLENGR 410
 QY 411 HLREYOYGLAMWRRRTTREATTELLGRLVLRMDMLGCLIEDIEALCGPALPAPASLL 470
 DB 411 HLREYOYGLAMWRRRTTREATTELLGRLVLRMDMLGCLIEDIEALCGPALPAPASLL 470
 QY 395 CLREAGYSLATWRRTTREATTELLGRLVLRMDMLGCLIEDIEALCGPALPAPASLL 454

RESULT 11

US-09-935-727-5
 ; Sequence 5, Application US/09935727
 ; Patent No. US20020150583A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
 ; FILE REFERENCE: PF454P2
 ; CURRENT APPLICATION NUMBER: US/09/935,727
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/303,224
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 60/252,131
 ; PRIOR FILING DATE: 2000-11-21
 ; PRIOR APPLICATION NUMBER: 60/227,598
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: 09/518,931
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: 60/166,235
 ; PRIOR FILING DATE: 1999-12-01
 ; PRIOR APPLICATION NUMBER: 60/146,371
 ; PRIOR FILING DATE: 1999-08-02
 ; PRIOR APPLICATION NUMBER: 60/131,964
 ; PRIOR FILING DATE: 1999-04-30
 ; PRIOR APPLICATION NUMBER: 60/131,270
 ; PRIOR FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: 60/124,092
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/121,774
 ; PRIOR FILING DATE: 1999-03-04
 ; PRIOR APPLICATION NUMBER: 09/006,352
 ; PRIOR FILING DATE: 1998-01-13
 ; PRIOR APPLICATION NUMBER: 60/035,496
 ; PRIOR FILING DATE: 1997-01-14
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 455
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 58.3%; Score 1517; DB 10; Length 455;

Best Local Similarity 62.9%; Pred. No. 7,1e-101; Mismatches 104; Indels 36; Gaps 7;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGILLPLVLPALADVYAGVGVPHPDLEKESPCPOGKYNHPONSTICT 60
 DB 1 MGLSTVPLDLLPLVLELVIGYPSGVIGLVPHLDREKRDVSCQGXIHPONSICT 60
 QY 61 KCHKGTLYNDGPGGDDTCRCESGSGFTASENHLRCLSCSKRKGQVEISSCTVD 120
 DB 61 KCHKGTLYNDGPGGDDTCRCESGSGFTASENHLRCLSCSKRKGQVEISSCTVD 120
 QY 121 RDTVCGCRKQYREYWGEGTGRCLNCSLCPNGTINIICOERODTICHGMGFLKAGACI 180
 DB 121 RDTVCGCRKQYREYWGEGTGRCLNCSLCPNGTINIICOERODTICHGMGFLKAGACI 180
 QY 121 RDTVCGCRKQYREYWGEGTGRCLNCSLCPNGTINIICOERODTICHGMGFLKAGACI 180
 DB 121 RDTVCGCRKQYREYWGEGTGRCLNCSLCPNGTINIICOERODTICHGMGFLKAGACI 180
 QY 181 SCHDCRNR-ECKELCPTRPSTGKSDOPGTTVLLPLVIVGCLASFAVYLACRYGRWK 239
 DB 181 SCHDCRNR-ECKELCPTRPSTGKSDOPGTTVLLPLVIVGCLASFAVYLACRYGRWK 239
 QY 181 SCHDCRNR-ECKELCPTRPSTGKSDOPGTTVLLPLVIVGCLASFAVYLACRYGRWK 239
 DB 181 SCHDCRNR-ECKELCPTRPSTGKSDOPGTTVLLPLVIVGCLASFAVYLACRYGRWK 239
 QY 240 PKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICSSSTPSSPVSIPT 290
 DB 240 PKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICSSSTPSSPVSIPT 290
 QY 241 SKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICSSSTPSSPVSIPT 300
 DB 241 SKLYSIICGOSTLVKEGEP-----LVVAPGFNP-----TTTICSSSTPSSPVSIPT 300
 QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
 DB 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
 QY 301 PGDCPNF---AARREVAAPYOGADPIL-----ATL-----ASDPI 335
 DB 301 PGDCPNF---AARREVAAPYOGADPIL-----ATL-----ASDPI 335
 QY 351 TPVQWEASAPADQADADPATLYAVVDGVPSSRWKELVRRIGLSEHEIERLENGR 410

Db 336 NPLQKMEBSA-HKQSLTDDPATLYAVENVPPRLKWEFVRRLGSLSEHIEDRLONGR 394
Qy 411 HUREAOYSMLAAMRRRTPRREATTLELGRVLRDMDLGLCLENIEBALGAARLASBPRL 470
Db 395 CLREAOYSMLATWRRRTPRREATTLELGRVLRDMDLGLCLENIEBALGPALPAPBPRL 454

RESULT 12

US-09-898-234-2
Sequence 2, Application US/09898234
Patent No. US20020155112A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Himmler, Adolph
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stralow, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
TITLE OF INVENTION: Them
FILE REFERENCE: 98,385-1
CURRENT FILING DATE: 2001-07-03
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 09/525,998
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-898-234-2

Query Match 58.3%; Score 1517; DB 10; Length 455;

Best Local Similarity 62.9%; Pred. No. 7.1e-101; Mismatches 104; Indels 36; Gaps 7;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPLLLPLVLRPALLADVPAGVGLVPHRPGDEKRESPPCGKYNPNSTICT 60
Db 1 MGLSTVPLLLPLVLRPALLADVPAGVGLVPHRPGDEKRESPPCGKYNPNSTICT 60
Qy 61 KCHGTYLYNDPCPGQDTPDCRECEGSGFTASBNHLRCLSCSKRCKEMGVETISSCTVD 120
Db 61 KCHGTYLYNDPCPGQDTPDCRECEGSGFTASBNHLRCLSCSKRCKEMGVETISSCTVD 120
Qy 121 RDTVCGGRKQRYRYWGTGTRCLNCSLCRNQNTVNIPOEROPTCHCHMGFFLKAGCT 180
Db 121 RDTVCGGRKQRYRYWGTGTRCLNCSLCRNQNTVNIPOEROPTCHCHMGFFLKAGCT 180
Qy 121 RDTVCGGRKQRYRYWGTGTRCLNCSLCRNQNTVNIPOEROPTCHCHMGFFLKAGCT 180
Db 121 RDTVCGGRKQRYRYWGTGTRCLNCSLCRNQNTVNIPOEROPTCHCHMGFFLKAGCT 180
Qy 181 SCHDCKNK-EECEKLCPTRPSTGKDSODPGTTVLLPLVIFGLCLASFASVVLACRYORWK 239
Db 181 SCHDCKNK-EECEKLCPTRPSTGKDSODPGTTVLLPLVIFGLCLASFASVVLACRYORWK 239
Qy 181 SCHDCKNK-EECEKLCPTRPSTGKDSODPGTTVLLPLVIFGLCLASFASVVLACRYORWK 239
Db 181 SCHDCKNK-EECEKLCPTRPSTGKDSODPGTTVLLPLVIFGLCLASFASVVLACRYORWK 239
Qy 240 PKLYSIICGOSTLVKEGEP-----LLVPAGFNP-----TTTICFSSSTPSSSPVSIPIYI 290
Db 240 PKLYSIICGOSTLVKEGEP-----LLVPAGFNP-----TTTICFSSSTPSSSPVSIPIYI 290
Qy 241 SKLYSIICGOSTLVKEGEP-----LLVPAGFNP-----TTTICFSSSTPSSSPVSIPIYI 300
Db 241 SKLYSIICGOSTLVKEGEP-----LLVPAGFNP-----TTTICFSSSTPSSSPVSIPIYI 300
Qy 291 SCDSNFGAASPSSETAPRLKAGPILPBPASTHLCTGPBPASTHLCTGPBPASTHLCT 350
Db 291 SCDSNFGAASPSSETAPRLKAGPILPBPASTHLCTGPBPASTHLCTGPBPASTHLCT 350
Qy 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATAL-----ASDPIP 335
Db 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVQKWEASAPASADOLADADPATLYAVVGVPPSRMKELVRRLGLSEHIERLENGR 410
Db 351 TPVQKWEASAPASADOLADADPATLYAVVGVPPSRMKELVRRLGLSEHIERLENGR 410
Qy 336 NPLQKMEBSA-HKQSLTDDPATLYAVENVPPRLKWEFVRRLGSLSEHIEDRLONGR 394
Db 336 NPLQKMEBSA-HKQSLTDDPATLYAVENVPPRLKWEFVRRLGSLSEHIEDRLONGR 394
Qy 411 HUREAOYSMLAAMRRRTPRREATTLELGRVLRDMDLGLCLENIEBALGAARLASBPRL 470
Db 411 HUREAOYSMLAAMRRRTPRREATTLELGRVLRDMDLGLCLENIEBALGAARLASBPRL 470

Db 395 CLREAOYSMLATWRRRTPRREATTLELGRVLRDMDLGLCLENIEBALGPALPAPBPRL 454

RESULT 13

US-09-898-234-17
Sequence 17, Application US/09898234
Patent No. US20020155112A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Himmler, Adolph
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stralow, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
TITLE OF INVENTION: Them
FILE REFERENCE: 98,385-1
CURRENT FILING DATE: 2001-07-03
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 09/525,998
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 455
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: human TNF-R in
OTHER INFORMATION: 1TNF-R2
US-09-898-234-17

Query Match 58.3%; Score 1517; DB 10; Length 455;

Best Local Similarity 62.9%; Pred. No. 7.1e-101; Mismatches 104; Indels 36; Gaps 7;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPLLLPLVLRPALLADVPAGVGLVPHRPGDEKRESPPCGKYNPNSTICT 60
Db 1 MGLSTVPLLLPLVLRPALLADVPAGVGLVPHRPGDEKRESPPCGKYNPNSTICT 60
Qy 61 KCHGTYLYNDPCPGQDTPDCRECEGSGFTASBNHLRCLSCSKRCKEMGVETISSCTVD 120
Db 61 KCHGTYLYNDPCPGQDTPDCRECEGSGFTASBNHLRCLSCSKRCKEMGVETISSCTVD 120
Qy 121 RDTVCGGRKQRYRYWGTGTRCLNCSLCRNQNTVNIPOEROPTCHCHMGFFLKAGCT 180
Db 121 RDTVCGGRKQRYRYWGTGTRCLNCSLCRNQNTVNIPOEROPTCHCHMGFFLKAGCT 180
Qy 121 RDTVCGGRKQRYRYWGTGTRCLNCSLCRNQNTVNIPOEROPTCHCHMGFFLKAGCT 180
Db 121 RDTVCGGRKQRYRYWGTGTRCLNCSLCRNQNTVNIPOEROPTCHCHMGFFLKAGCT 180
Qy 181 SCHDCKNK-EECEKLCPTRPSTGKDSODPGTTVLLPLVIFGLCLASFASVVLACRYORWK 239
Db 181 SCHDCKNK-EECEKLCPTRPSTGKDSODPGTTVLLPLVIFGLCLASFASVVLACRYORWK 239
Qy 181 SCHDCKNK-EECEKLCPTRPSTGKDSODPGTTVLLPLVIFGLCLASFASVVLACRYORWK 239
Db 181 SCHDCKNK-EECEKLCPTRPSTGKDSODPGTTVLLPLVIFGLCLASFASVVLACRYORWK 239
Qy 240 PKLYSIICGOSTLVKEGEP-----LLVPAGFNP-----TTTICFSSSTPSSSPVSIPIYI 290
Db 240 PKLYSIICGOSTLVKEGEP-----LLVPAGFNP-----TTTICFSSSTPSSSPVSIPIYI 290
Qy 241 SKLYSIICGOSTLVKEGEP-----LLVPAGFNP-----TTTICFSSSTPSSSPVSIPIYI 300
Db 241 SKLYSIICGOSTLVKEGEP-----LLVPAGFNP-----TTTICFSSSTPSSSPVSIPIYI 300
Qy 291 SCDSNFGAASPSSETAPRLKAGPILPBPASTHLCTGPBPASTHLCTGPBPASTHLCT 350
Db 291 SCDSNFGAASPSSETAPRLKAGPILPBPASTHLCTGPBPASTHLCTGPBPASTHLCT 350
Qy 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATAL-----ASDPIP 335
Db 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVQKWEASAPASADOLADADPATLYAVVGVPPSRMKELVRRLGLSEHIERLENGR 410
Db 351 TPVQKWEASAPASADOLADADPATLYAVVGVPPSRMKELVRRLGLSEHIERLENGR 410
Qy 336 NPLQKMEBSA-HKQSLTDDPATLYAVENVPPRLKWEFVRRLGSLSEHIEDRLONGR 394
Db 336 NPLQKMEBSA-HKQSLTDDPATLYAVENVPPRLKWEFVRRLGSLSEHIEDRLONGR 394
Qy 411 HUREAOYSMLAAMRRRTPRREATTLELGRVLRDMDLGLCLENIEBALGAARLASBPRL 470
Db 411 HUREAOYSMLAAMRRRTPRREATTLELGRVLRDMDLGLCLENIEBALGAARLASBPRL 470

DB 395 CLREAQVSMLATWRRRTPREATLELLGCVLRDMDLGLCLEDIEBALCGPALPPAPSL 454

RESULT 14
US-09-756-854-5
Sequence 5, Application US/09756854
Patent No. US20020164684A1
GENERAL INFORMATION:
APPLICANT: NI, Jian
Yu, Guo-Liang
Fan, Ping
Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,094
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-756-854-5

Query Match 58.3%; Score 1517; DB 10; Length 455;
Best Local Similarity 62.9%; Pred. No. 7,1e-101;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGLLPLVLPALADVPAGVGLVPHPDLEKRESPPCGQKYNHPNSTICT 60
DB 1 MGLSTVPLLLPLVLELVGIVPSGVGLVPHLCDEKRSVCGQKYNHPNSTICT 60
QY 61 KCHKGTLYNDCPGRGRTDRCVCAPTVTLLENHRLRCLSCSRDRMPVEISPCVVD 120
DB 61 KCHKGTLYNDCPGRGRTDRCVCAPTVTLLENHRLRCLSCSRDRMPVEISPCVVD 120
QY 121 RDTVCGCKNOYREXWGTGFRCLNCSLCPNGTNNIPCOERDPTICHGMGFFLGAKCI 180
DB 121 RDTVCGCKNOYREXWGTGFRCLNCSLCPNGTNNIPCOERDPTICHGMGFFLGAKCI 180
QY 181 SCHDCKN-EECKLCPTRPSTGKSDODPGTTVLLPLVIVFGCLASFASVVLACRYQRM 239
DB 181 SCHDCKN-EECKLCPTRPSTGKSDODPGTTVLLPLVIVFGCLASFASVVLACRYQRM 239
QY 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSTPSSSPVSIPIYI 290
DB 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSTPSSSPVSIPIYI 290
QY 241 SKLYSIVCGKSTPEKEGLEGTTRTKPLAPNPSFSTPGFTTLGSPVPSSTFTSSSTYT 300
DB 241 SKLYSIVCGKSTPEKEGLEGTTRTKPLAPNPSFSTPGFTTLGSPVPSSTFTSSSTYT 300

QY 291 SCDNSNFCAVASPSSETAPPHLKAGPLIGPPASTHLCCTGPPASTHLCCTGPPASTHLC 350
DB 301 PGDCPNF---AAPREVAPPYQADPIL-----ATAL-----ASDIP 335
QY 351 TPVQKWEASAPSDQDLADADPATLYAVVDDVPSPRWELVRLGLSEHIERLENGR 410
DB 351 TPVQKWEASAPSDQDLADADPATLYAVVDDVPSPRWELVRLGLSEHIERLENGR 410
QY 394 NPLQKWEASA-HKPGSLTDTPATLYAVVENVPPLRWKEPFRRLGSLDHEIDRLBLQNGR 394
DB 395 CLREAQVSMLATWRRRTPREATLELLGCVLRDMDLGLCLEDIEBALCGPALPPAPSL 454

RESULT 15
US-09-899-429A-2
Sequence 2, Application US/09899429A
Patent No. US20020169118A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
Himmeler, Adolph
Maurer-Fogay, Ingrid
APPLICANT: Stralowa, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
FILE REFERENCE: 98-385-J
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,429A
FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/792,356
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.0
LENGTH: 455
SEQ ID NO 2
TYPE: PRT
ORGANISM: Homo sapiens
US-09-899-429A-2

Query Match 58.3%; Score 1517; DB 10; Length 455;
Best Local Similarity 62.9%; Pred. No. 7,1e-101;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPGLLPLVLPALADVPAGVGLVPHPDLEKRESPPCGQKYNHPNSTICT 60
DB 1 MGLSTVPLLLPLVLELVGIVPSGVGLVPHLCDEKRSVCGQKYNHPNSTICT 60
QY 61 KCHKGTLYNDCPGRGRTDRCVCAPTVTLLENHRLRCLSCSRDRMPVEISPCVVD 120
DB 61 KCHKGTLYNDCPGRGRTDRCVCAPTVTLLENHRLRCLSCSRDRMPVEISPCVVD 120
QY 121 RDTVCGCKNOYREXWGTGFRCLNCSLCPNGTNNIPCOERDPTICHGMGFFLGAKCI 180
DB 121 RDTVCGCKNOYREXWGTGFRCLNCSLCPNGTNNIPCOERDPTICHGMGFFLGAKCI 180
QY 181 SCHDCKN-EECKLCPTRPSTGKSDODPGTTVLLPLVIVFGCLASFASVVLACRYQRM 239
DB 181 SCHDCKN-EECKLCPTRPSTGKSDODPGTTVLLPLVIVFGCLASFASVVLACRYQRM 239
QY 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSTPSSSPVSIPIYI 290
DB 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSTPSSSPVSIPIYI 290
QY 241 SKLYSIVCGKSTPEKEGLEGTTRTKPLAPNPSFSTPGFTTLGSPVPSSTFTSSSTYT 300
DB 241 SKLYSIVCGKSTPEKEGLEGTTRTKPLAPNPSFSTPGFTTLGSPVPSSTFTSSSTYT 300

Db	301	PGDCPNF--AAPRREVAFPYOGADPIL-----ATAL-----ASDPIL	335
Qy	351	TPVQKWEASAPSPADQADADPATLYAVVDGVPSPRWKELVRRLGISEHEIERLENGR	410
Db	336	NPLQKWEDSA-HKPSLDTDDPATLYAVVENVPPLRWKEFVRRLGSDHEIDRIELONGR	394
Qy	411	HLREAOYSMLAAMRRRTTPREATTLELGRVLRDMDLGCLENIEBALGGAARLASERLL	470
Db	395	CLREAOYSMLATWRRTTPREATTLELGRVLRDMDLGCLEDBBALCGPAALPPAPSL	454

Search completed: September 13, 2003, 07:10:54
 Job time : 28 secs

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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:02:24 / Search time 20 Seconds

(without alignments)
2264.772 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603
Sequence: 1 MGLPTVPGLLPLVLPALLA.....NIEBALGCAARLASPPRLW 471

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR_76:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1750	67.2	461	2	JC4302 tumor necrosis fac
2	1517	58.3	455	1	GQHUT1 tumor necrosis fac
3	1338.5	51.4	461	1	GQRTT1 tumor necrosis fac
4	1319	50.7	454	1	GQNST1 tumor necrosis fac
5	257	9.9	435	2	IS4182 tumor necrosis fac
6	236	9.1	427	1	GQHUN tumor necrosis fac
7	227.5	8.7	425	1	A26431 nerve growth facto
8	220	8.5	416	1	JN0006 nerve growth facto
9	199.5	7.7	451	2	JC7705 death receptor-6 -
10	199	7.6	461	1	A35356 tumor necrosis fac
11	193	7.4	595	2	A42086 CD30 antigen precu
12	181.5	7.0	324	2	JC2395 Fas antigen precu
13	181.5	7.0	325	2	B43692 T2 protein - rabbi
14	180	6.9	326	1	GQVZML T2 protein - myom
15	178.5	6.9	474	2	B38634 tumor necrosis fac
16	173	6.6	459	2	I48854 gene murine tumor
17	169	6.5	3635	2	T10053 laminin alpha 5 ch
18	168.5	6.5	305	2	A46476 B cell-associated
19	163.5	6.3	348	2	J28623 hypothetical prote
20	163.5	6.3	349	2	D72175 G2R protein - vari
21	163.5	6.3	349	2	D36858 gene GAR protein -
22	161	6.2	327	2	A46484 apoptosis-mediatin
23	155	6.0	1548	2	S34583 serine proteinase
24	150	5.8	1613	2	JB0272 low density lipopr
25	149	5.7	1613	2	JB0273 laminin beta-2 cha
26	147.5	5.7	1801	1	MRRTS apoptosis-mediatin
27	147	5.6	335	2	A40036 notch3 protein - h
28	147	5.6	2321	2	S78549 furin (EC 3.4.21.7
29	145.5	5.6	1299	2	T43251

30	145	5.6	260	1	A46517 CD27 antigen precu
31	142.5	5.5	1639	1	MMFR2 laminin gamma-1 ch
32	141.5	5.4	915	2	B48225 probable propterei
33	140.5	5.4	1111	2	T26972 hypothetical prote
34	140.5	5.4	1513	2	A54895 mucin 2, intestina
35	140.5	5.4	3020	2	A43932 mucin 2 precursor,
36	140	5.4	277	2	I37552 OX40 homolog - hum
37	140	5.4	1797	2	A55677 laminin beta-2 cha
38	139.5	5.4	3672	2	T23433 hypothetical prote
39	139.5	5.4	3704	2	T73316 probable laminin a
40	138.5	5.3	915	1	A48225 subtilisin-like pr
41	138	5.3	5262	2	T03454 AAR protein - huma
42	137.5	5.3	1574	2	T13954 MGCF6 protein - ra
43	137.5	5.3	5376	2	T42215 zonadhesin - mouse
44	136	5.2	826	2	A60385 monocyte surface a
45	135.5	5.2	937	2	I53282 gene PAC4 protein

ALIGNMENTS

RESULT 1

JC4302 tumor necrosis factor receptor p55 precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 29-Nov-1995 #sequence #revision 08-Feb-1996 #text_change 23-Jul-1999

C:Accession: JC4302; PC4093

R:Stuer, B.; Pauli, U

A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

A:Reference number: JC4302; MUID:96011645; PMID:7590278

A:Accession: JC4302

A:Molecule type: mRNA

A:Residues: 1-461 <SU2>

A:Cross-references: GB:U1994; MID:g1141752; PIDN:AN048499.1; PID:g1141753

A:Accession: PC4093

A:Molecule type: protein

A:Residues: 1-7 <SU2>

A:Experimental source: kidney cell line 15

C:Genetics:

A:Gene: tnfr

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>

F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>

F:84-126/Domain: NGF receptor repeat homology <NGF>

F:211-231/Domain: transmembrane #status predicted <TM>

F:361-447/Domain: signal transduction #status predicted <ST>

F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.2% Score 1750; DB 2; Length 461;

Best Local Similarity 70.2% Pred. No. 6.5e-100;

Matches 339; Conservative 24; Mismatches 84; Indels 36; Gaps 5;

QY	1	MGLPTVPGLLPLVLPALLADVPAVGGLVPHPGDLEKRRSPQCKRVNPNSTICT	60
DB	1	MGLSTVPGLLPLVLPALLDVPAVGHGLVHGDDEKRSLCPQGRTHPNRSLICT	60
QY	61	KCHGTYLVNDPCPGRDTCRCVAPGTATLENHLRRCSCSRQDPMQVEISPCVD	120
DB	61	KCHGTYLVNDPCPGDTCRCVAPGTATLENHLRRCSCSRQDPMQVEISPCVD	120
QY	121	RDYVCGCRKQYRYWGTGRCLNSCLPNGTNNPCOEODITICCHMGFLKAKCI	180
DB	121	RDYVCGCRKQYRYWGTGRCLNSCLPNGTNNPCOEODITICCHMGFLKAKCI	180
QY	181	SCHDCKNECEKLCPTPSTGSDQDGTITVLPLVIVFGCLASFASVYLACGYORKKP	240
DB	181	SCVCKNADCKNLCPATSETRNDPDGTITVLPLVIVFGCLASFFLVGLACGYORKKP	240
QY	241	KLVSIIIGOSTLVKGEPELLVPAQGNPTT-----CFSSSTPSSSPVSIPIYI	290

Db 241 KLVSTICGKSTVXGGEPEPLATAPSPGPITTFSPSPPTTSSPVSPSPSPPT 300
 Qy 231 SCDRNFGAVASPSSETAPPHKAGPILFGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
 Db 301 PCDMNMI-KVSPSPPEIAPPPGAGPILPMPAS-----TPVP----- 337
 Qy 351 TPVQKMEA---SAPAPDQADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLELE 407
 Db 338 TPLPMGSAHSAHAPQADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLELE 397
 Qy 408 NGRHLREAOYSMLAAMRRRTPRREATLELGLVRLDMDLGLCLENIEEALGGAALAEAP 467
 Db 398 NGRCLREAOYSMLAAMRRRTSRREATLELGLVRLDMDLGLCLENIEEALGGAALAEAP 457
 Qy 468 RLL 470
 Db 458 HLL 460

RESULT 2

NUMOT1
 tumor necrosis factor receptor 1 precursor [validated] - human
 M:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
 N:Contactus: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence revision 30-Jun-1992 #text change 08-Dec-2000
 C:Accession: A38208; A34899; A34900; A36555; A38281; S12057; J07058; A60231; A38
 R:Funcs: P.; Strehl, S.; Dwozrak, M.; Himmler, A.; Ambrose, P.F.
 Genomic 13, 219-224, 1992
 A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to ch
 A:Reference number: A38208; PMID:92250049; PMID:1315717
 A:Accession: A38208
 A:Molecule type: DNA
 A:Residues: 1-455 <FUC>
 A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:G339748; PIDN:AAA61201.1; PID:G
 R:Loebercher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau
 Cell 61, 351-359, 1990
 A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep
 A:Reference number: A34899; PMID:90235284; PMID:2158862
 A:Accession: A34899
 A:Molecule type: mRNA
 A:Residues: 1-455 <LOB>
 A:Cross-references: GB:M58286; GB:M3480; NID:G339753; PIDN:AAA36753.1; PID:G339754
 A:Experimental source: placenta
 A:Note: part of this sequence, including the amino end of the mature protein, confirmed
 R:Schall, T.J.; Lewis, M.; Koller, K.D.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.
 Cell 61, 361-370, 1990
 A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor
 A:Reference number: A34900; PMID:90235285; PMID:2158863
 A:Accession: A34900
 A:Molecule type: mRNA
 A:Residues: 1-455 <SCH>
 A:Cross-references: GB:M3294; NID:G339744; PIDN:AAA03210.1; PID:G339745
 R:Himmler, A.; Maunier-Fogay, I.; Kronke, M.; Scheutrich, P.; Pfizenmaier, K.; Lantz, M.;
 DNA Cell Biol. 9, 705-715, 1990
 A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
 A:Reference number: A36555; PMID:91090841; PMID:1702293
 A:Accession: A36555
 A:Molecule type: mRNA
 A:Residues: 1-455 <HIM>
 A:Cross-references: GB:M63121; NID:G339755; PIDN:AAA36754.1; PID:G339756
 A:Accession: C36555
 A:Molecule type: protein
 A:Residues: 30-38/41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104/107-128/162-167, 'X', 169-2
 A:Note: the purified protein, called tumor necrosis factor binding protein, is a soluble
 R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
 A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re
 A:Reference number: A38281; PMID:91017509; PMID:2170974
 A:Accession: A38281
 A:Molecule type: mRNA
 A:Residues: 1-455 <GRA>

A:Cross-references: GB:M37764
 A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
 R:Nopht, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zhang, R.; Aderka, D.; Holtmann,
 EMBO J. 9, 3269-3278, 1990
 A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
 le form of the receptor.
 A:Reference number: S12057; PMID:9106021; PMID:1698610
 A:Accession: S12057
 A:Molecule type: mRNA
 A:Residues: 1-455 <NOP>
 A:Cross-references: EMBL:X53113; NID:G37223; PIDN:CAA39021.1; PID:G37224
 A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, we
 R:Kemper, O.; Wallach, D.
 Gene 134, 209-216, 1993
 A:Title: Cloning and partial characterization of the promoter for the human p55 tumor nec
 A:Reference number: J07058; PMID:94085779; PMID:8262379
 A:Accession: J07058
 A:Molecule type: DNA
 A:Residues: 1-13 <KEM>
 R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
 Eur. J. Immunol. 20, 1167-1174, 1990
 A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence
 A:Reference number: A60231; PMID:90292116; PMID:2113477
 A:Accession: A60231
 A:Molecule type: protein
 A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
 R:Gatanaga, T.; Huang, C.; Kohr, W.; Capucci, F.; Lucchi III, J.A.; Jeffee, E.W.B.; Le
 Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
 A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor)
 A:Reference number: A38258; PMID:91062364; PMID:2174164
 A:Accession: A38258
 A:Molecule type: protein
 A:Residues: 41-60 <GAT>
 A:Experimental source: cancer patient serum
 R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyrell, H.; Grubb, A.; Adolf, G.
 Eur. J. Haematol. 42, 270-275, 1989
 A:Title: Isolation and characterization of a tumor necrosis factor binding protein from
 A:Reference number: A60594; PMID:89171156; PMID:2924890
 A:Accession: A60594
 A:Molecule type: protein
 A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>
 A:Experimental source: renal failure patient urine
 R:Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence f
 A:Reference number: A35010; PMID:90110215; PMID:2153136
 A:Accession: A35010
 A:Molecule type: protein
 A:Residues: 41-45 <ENG>
 A:Experimental source: normal urine
 R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
 Bioest. Biotechnol. Biochem. 58, 2266-2268, 1994
 A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified fr
 A:Reference number: J02404; PMID:95128033; PMID:7765720
 A:Accession: J02404
 A:Molecule type: protein
 A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAL>
 A:Experimental source: urine
 C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
 C:Genetics:
 A:Gene: GDB:TNFR1
 A:Cross-references: GDB:125913; OMIM:191190
 A:Map position: 12p13.2-12p13.2
 A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
 F:30-211/Domain: extracellular #status predicted <EXT>
 F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
 F:44-82/Domain: NGF receptor repeat homology <NG1>
 F:84-126/Domain: NGF receptor repeat homology <NG2>

F:127-167/Domain: NGF receptor repeat homology <NG3>
 F:168-196/Domain: NGF receptor repeat homology <NG4>
 F:212-234/Domain: transmembrane #status predicted <MEM>
 F:235-455/Domain: intracellular #status predicted <INT>
 F:54,145,151/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.3%; Score 1517; DB 1; Length 455;
 Best Local Similarity 62.9%; Pred. No. 1,1e-85;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGSLPTVGLLPLVLPALLADVPAGVQGLVPHRGDLKRESPCKQKXHPONSTICT 60
 DB 1 MGSLPTVGLLPLVLPALLADVPAGVQGLVPHRGDLKRESPCKQKXHPONSTICT 60
 QY 61 KCHKGTLYNDCEPGRDTCRCVCAPTVTALBNHLRCLSCSRCDREMFVEISPCVD 120
 DB 61 KCHKGTLYNDCEPGRDTCRCVCAPTVTALBNHLRCLSCSRCDREMFVEISPCVD 120
 QY 121 RDTVCGCRKQRYREYWGCTFRCLNSLCPNGVTNIPQERQDTTICCHMGFFLKAKCI 180
 DB 121 RDTVCGCRKQRYREYWGCTFRCLNSLCPNGVTNIPQERQDTTICCHMGFFLKAKCI 180
 QY 181 SCHDCRKK-ECEKICPTRPSTGKDSODPGTTLPLVTYVGLCLASPASVYLACRYORWK 239
 DB 181 SCHDCRKK-ECEKICPTRPSTGKDSODPGTTLPLVTYVGLCLASPASVYLACRYORWK 239
 QY 240 PKLYSIICGOSTLVKEGEPE-----LVPAPGFNP-----TTTICFSSSTPSSPVSIIPPYI 290
 DB 240 PKLYSIICGOSTLVKEGEPE-----LVPAPGFNP-----TTTICFSSSTPSSPVSIIPPYI 290
 QY 291 SCDSNFGAVASPSSETAPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 DB 291 SCDSNFGAVASPSSETAPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 QY 301 PGDCPNF---AAPREVAPPYGADPIL-----ATML-----ASDPFIP 335
 DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATML-----ASDPFIP 335
 QY 351 TPVQKWEASASAPDOLADAPATLYAVDGPSPKWEKLVRLGLSHEHELELENGR 410
 DB 351 TPVQKWEASASAPDOLADAPATLYAVDGPSPKWEKLVRLGLSHEHELELENGR 410
 QY 393 NPLQKWEASA-HKQSLDTPDPAFLYAVENVPLPKWEKLVRLGLSHEHELELENGR 394
 DB 393 NPLQKWEASA-HKQSLDTPDPAFLYAVENVPLPKWEKLVRLGLSHEHELELENGR 394
 QY 411 HLRAQXSMLAAMRRRTPRRATLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 470
 DB 411 HLRAQXSMLAAMRRRTPRRATLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 470
 QY 454 CLRAQXSMLAAMRRRTPRRATLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 454
 DB 454 CLRAQXSMLAAMRRRTPRRATLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 454

RESULT 3

GOMST1

tumor necrosis factor receptor 1 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999

R:Hitmiller, A.; Maurer-Fogy, I.; Kroenke, M.; Scheutrich, P.; Pitzemaier, K.; Lantz, M.; DNA Cell Biol. 9, 705-715, 1990

A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor

A:Reference number: A36555; MUID:91090841; PMID:1702293

A:Accession: B36555

A:Molecule type: mRNA

A:Residues: 1-461 <HIM>

A:Cross-references: GB:M63122; NID:9207361; PIDN:AAA42256.1; PID:9207362

C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-461/Domain: signal sequence #status predicted <SIG>

F:30-201/Domain: extracellular #status predicted <EXT>

F:30-201/Domain: extracellular #status predicted <EXT>

F:30-201/Domain: extracellular #status predicted <EXT>

Query Match 51.4%; Score 1338.5; DB 1; Length 461;
 Best Local Similarity 55.8%; Pred. No. 9.2e-75;
 Matches 268; Conservative 51; Mismatches 114; Indels 47; Gaps 9;

QY 1 MGSLPTVGLLPLVLPALLADVPAGVQGLVPHRGDLKRESPCKQKXHPONSTICT 60
 DB 1 MGSLPTVGLLPLVLPALLADVPAGVQGLVPHRGDLKRESPCKQKXHPONSTICT 60
 QY 61 KCHKGTLYNDCEPGRDTCRCVCAPTVTALBNHLRCLSCSRCDREMFVEISPCVD 120
 DB 61 KCHKGTLYNDCEPGRDTCRCVCAPTVTALBNHLRCLSCSRCDREMFVEISPCVD 120
 QY 121 RDTVCGCRKQRYREYWGCTFRCLNSLCPNGVTNIPQERQDTTICCHMGFFLKAKCI 180
 DB 121 RDTVCGCRKQRYREYWGCTFRCLNSLCPNGVTNIPQERQDTTICCHMGFFLKAKCI 180
 QY 181 SCHDCRKK-ECEKICPTRPSTGKDSODPGTTLPLVTYVGLCLASPASVYLACRYORWK 239
 DB 181 SCHDCRKK-ECEKICPTRPSTGKDSODPGTTLPLVTYVGLCLASPASVYLACRYORWK 239
 QY 240 PKLYSIICGOSTLVKEGEPE-----LVPAPGFNP-----TTTICFSSSTPSSPVSIIPPYI 290
 DB 240 PKLYSIICGOSTLVKEGEPE-----LVPAPGFNP-----TTTICFSSSTPSSPVSIIPPYI 290
 QY 291 SCDSNFGAVASPSSETAPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 DB 291 SCDSNFGAVASPSSETAPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 QY 301 PGDCPNF---AAPREVAPPYGADPIL-----ATML-----ASDPFIP 335
 DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATML-----ASDPFIP 335
 QY 351 TPVQKWEASASAPDOLADAPATLYAVDGPSPKWEKLVRLGLSHEHELELENGR 410
 DB 351 TPVQKWEASASAPDOLADAPATLYAVDGPSPKWEKLVRLGLSHEHELELENGR 410
 QY 393 NPLQKWEASA-HKQSLDTPDPAFLYAVENVPLPKWEKLVRLGLSHEHELELENGR 394
 DB 393 NPLQKWEASA-HKQSLDTPDPAFLYAVENVPLPKWEKLVRLGLSHEHELELENGR 394
 QY 402 ERLELENGRHLRAQXSMLAAMRRRTPRRATLELGRVLRDMDLGLCLENIEBALGGA 461
 DB 402 ERLELENGRHLRAQXSMLAAMRRRTPRRATLELGRVLRDMDLGLCLENIEBALGGA 461
 QY 452 ERLELENGRHLRAQXSMLAAMRRRTPRRATLELGRVLRDMDLGLCLENIEBALGGA 452
 DB 452 ERLELENGRHLRAQXSMLAAMRRRTPRRATLELGRVLRDMDLGLCLENIEBALGGA 452

RESULT 4

GOMST1

tumor necrosis factor receptor 1 precursor - mouse

N:Alternate names: tumor necrosis factor receptor, 55K

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000

C:Accession: A38634; B40254; S16677; S19021; I54532; I57826

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.; Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r

A:Reference number: A38634; MUID:91187885; PMID:1849278

A:Accession: A38634

A:Molecule type: mRNA

A:Residues: 1-454 <LEW>

A:Cross-references: GB:M60468; NID:919825; PIDN:AAA39751.1; PID:919826

C:Comment: References: GB:M60468; NID:919825; PIDN:AAA39751.1; PID:919826

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-461/Domain: signal sequence #status predicted <SIG>

F:30-201/Domain: extracellular #status predicted <EXT>

F:30-201/Domain: extracellular #status predicted <EXT>

F:30-201/Domain: extracellular #status predicted <EXT>

F:30-201/Domain: extracellular #status predicted <EXT>

F:30-201/Domain: extracellular #status predicted <EXT>

A/Molecule type: mRNA
 A/Residues: 1-454 <ROT>
 A/Cross-references: EMBL:X57796; NID:G54848; PIDN:CAA40936.1; PID:G54849
 R/Rebo, B.P.
 Immunogenetics 39, 450-451, 1994
 A/Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1
 A/Reference number: 154533; MUID:94245292; PMID:8188324
 A/Accession: 154532
 A/Molecule type: mRNA
 A/Status: translated from GB/EMBL/DBJ
 A/Residues: 1-454 <RES>
 A/Cross-references: GB:126349; NID:9430732; PIDN:AAA59361.1; PID:9430733
 R/Rothe, J.G.; Blumhenn, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
 Mol. Immunol. 30, 165-176, 1993
 A/Title: Genome organization and promoter function of the murine tumor necrosis factor
 A/Reference number: 157826; MUID:93156721; PMID:8381516
 A/Accession: 157826
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-393; G', 395-454 <RES>
 A/Cross-references: GB:M76566; NID:9202100; PIDN:AAA40465.1; PID:9202102
 C/Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
 A/Gene: TNFR-2
 A/Intron: 13/3; 65/1; 108/1; 184/2; 210/1; 248/1; 257/3; 353/1
 C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C/Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei
 F.1-29/Domain: signal sequence #status predicted <SIG>
 F.30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
 F.30-212/Domain: extracellular #status predicted <EXT>
 F.44-82/Domain: NGF receptor repeat homology <NG1>
 F.84-126/Domain: NGF receptor repeat homology <NG2>
 F.127-167/Domain: NGF receptor repeat homology <NG3>
 F.168-204/Domain: NGF receptor repeat homology <NG4>
 F.213-235/Domain: transmembrane #status predicted <MEM>
 F.235-455/Domain: intracellular #status predicted <INT>
 F.54; 151; 202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.7%; Score 1319; DB 1; Length 454;
 Best Local Similarity 56.5%; Pred. No. 1,4e-73;
 Matches 268; Conservative 55; Mismatches 109; Indels 42; Gaps 12;

```

OY 1 MGLPVPGLLPLVLPALADYVPAVOGLVPHPDLEKRSPPQKYNHPONITICT 60
DB 1 MGLPVPGLLPLVLPALADYVPAVOGLVPHPDLEKRSPPQKYNHPONITICT 60
OY 1 MGLPVPGLLPLVLPALADYVPAVOGLVPHPDLEKRSPPQKYNHPONITICT 60
DB 1 MGLPVPGLLPLVLPALADYVPAVOGLVPHPDLEKRSPPQKYNHPONITICT 60
OY 61 KCHKSTVLYNDGPGRDTCVCAPGYTALENLARECLSGSRDDEMFOYEISPCYVD 120
DB 61 KCHKSTVLYNDGPGRDTCVCAPGYTALENLARECLSGSRDDEMFOYEISPCYVD 120
OY 61 KCHKSTVLYNDGPGRDTCVCAPGYTALENLARECLSGSRDDEMFOYEISPCYVD 120
DB 61 KCHKSTVLYNDGPGRDTCVCAPGYTALENLARECLSGSRDDEMFOYEISPCYVD 120
OY 121 RDTVGGCKRNOYREYMGSTGFRCLNCSLCPNGTVNI PCOERODTI CHGMEGFLKAKCI 180
DB 121 RDTVGGCKRNOYREYMGSTGFRCLNCSLCPNGTVNI PCOERODTI CHGMEGFLKAKCI 180
OY 121 RDTVGGCKRNOYREYMGSTGFRCLNCSLCPNGTVNI PCOERODTI CHGMEGFLKAKCI 180
DB 121 RDTVGGCKRNOYREYMGSTGFRCLNCSLCPNGTVNI PCOERODTI CHGMEGFLKAKCI 180
OY 181 SCHDC-KKKECEKLC-PTRPSTGKDSORPGTIVLLPLVIVFGCLASPAVVLACRYORW 238
DB 181 SCHDC-KKKECEKLC-PTRPSTGKDSORPGTIVLLPLVIVFGCLASPAVVLACRYORW 238
OY 181 SCHDC-KKKECEKLC-PTRPSTGKDSORPGTIVLLPLVIVFGCLASPAVVLACRYORW 238
DB 181 SCHDC-KKKECEKLC-PTRPSTGKDSORPGTIVLLPLVIVFGCLASPAVVLACRYORW 238
OY 181 PSCHCKKNEECCKLCLPPLPLAVNTPDOSTAIVLLPLVILGLCLISLFIPLSLMKRYRWM 240
DB 181 PSCHCKKNEECCKLCLPPLPLAVNTPDOSTAIVLLPLVILGLCLISLFIPLSLMKRYRWM 240
OY 239 KPLYSIICGOSTLVKE---GEPELLVPAPGFNPT-----TICGSSSTSSSPVSIPIYIS 291
DB 239 KPLYSIICGOSTLVKE---GEPELLVPAPGFNPT-----TICGSSSTSSSPVSIPIYIS 291
OY 241 RPEVYSIICRDPVPVPEKEKAKGKPLTPASPAFSPISGPNPLIGSTPSSPSSVSTP--- 297
DB 241 RPEVYSIICRDPVPVPEKEKAKGKPLTPASPAFSPISGPNPLIGSTPSSPSSVSTP--- 297
OY 292 CDRNFGAVAPSSSETAPPHLKAQILPGPASTHLCTPG--PPASTHLCT-PGPASTH 348
DB 292 CDRNFGAVAPSSSETAPPHLKAQILPGPASTHLCTPG--PPASTHLCT-PGPASTH 348
OY 298 -----ISPIFGPSNW-----HFM-----PVSSEVVPQAGADPLVYESLGVAP- 336
DB 298 -----ISPIFGPSNW-----HFM-----PVSSEVVPQAGADPLVYESLGVAP- 336
OY 349 LCTPVQKEASA-PSAPQLADADPATIYAVVDGVPBKRKVELVRLKLSHEIRLE 407
DB 349 LCTPVQKEASA-PSAPQLADADPATIYAVVDGVPBKRKVELVRLKLSHEIRLE 407
OY 337 --TSVQKEDSAHPRPD--NADAILYAVVDGVPBKRKVELVRLKLSHEIRLEMO 391
DB 337 --TSVQKEDSAHPRPD--NADAILYAVVDGVPBKRKVELVRLKLSHEIRLEMO 391
OY 408 NGRHLREAYQSMAMRRRTPREATLELGRVLDMDLCLCLEIIEALGAA 461
DB 408 NGRHLREAYQSMAMRRRTPREATLELGRVLDMDLCLCLEIIEALGAA 461
OY 392 NGRCLREAYQSMAMRRRTPREATLELGRVLDMDLCLCLEIIEALGAA 445
DB 392 NGRCLREAYQSMAMRRRTPREATLELGRVLDMDLCLCLEIIEALGAA 445

```

RESULT 5
 154182
 tumor necrosis factor receptor 2-related protein - human
 C/Species: Homo sapiens (man)
 C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
 C/Accession: 154182
 R/Baens, M.; Chalfanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
 Genomics 16, 214-218, 1993
 A/Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
 A/Reference number: 154182; MUID:93252381; PMID:8466360
 A/Accession: 154182
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-435 <RES>
 A/Cross-references: GB:L04270; NID:G339761; PIDN:AAA36757.1; PID:G339762
 C/Genetics:
 A/Gene: GDB:UTBR
 A/Cross-references: GDB:1230195; OMIM:600979
 A/Map position: 12p13.3-12p13.1
 C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 9.9%; Score 257; DB 2; Length 435;
 Best Local Similarity 27.3%; Pred. No. 1.1e-08;
 Matches 121; Conservative 37; Mismatches 158; Indels 128; Gaps 25;

```

OY 1 MGLP---TVPGLL-PLVLP--ALLADYVPAVOGLVPHPDLEKRSPPQKYNHPON 54
DB 1 MGLP---TVPGLL-PLVLP--ALLADYVPAVOGLVPHPDLEKRSPPQKYNHPON 54
OY 1 MGLP---TVPGLL-PLVLP--ALLADYVPAVOGLVPHPDLEKRSPPQKYNHPON 54
DB 1 MGLP---TVPGLL-PLVLP--ALLADYVPAVOGLVPHPDLEKRSPPQKYNHPON 54
OY 55 STICCKHKTLYLYNDGPGRDTCVCAPGYTALENLARECLSGSRDDEMFOYEI 114
DB 55 STICCKHKTLYLYNDGPGRDTCVCAPGYTALENLARECLSGSRDDEMFOYEI 114
OY 56 -RITCSRPPEPTVYSKAC-SRIKDTVCATCENSYNEMHNLITTCQCRPCDPVGLKEI 113
DB 56 -RITCSRPPEPTVYSKAC-SRIKDTVCATCENSYNEMHNLITTCQCRPCDPVGLKEI 113
OY 115 SPVVDVDTVGGCKRNOYREYMGSTGFRCLNCSL---CPNGTVNI PCOERODTI----- 165
DB 115 SPVVDVDTVGGCKRNOYREYMGSTGFRCLNCSL---CPNGTVNI PCOERODTI----- 165
OY 114 APCTSKRTQCRCPGMFCAM---ALECTHCELLSCPEPTE---ALEKDEVKGNH 166
DB 114 APCTSKRTQCRCPGMFCAM---ALECTHCELLSCPEPTE---ALEKDEVKGNH 166
OY 166 -CHCHMGFFLK---GAKCISCHCKKKECKLCP---TRPSTGKSDP-----GT-- 209
DB 166 -CHCHMGFFLK---GAKCISCHCKKKECKLCP---TRPSTGKSDP-----GT-- 209
OY 167 CVPKAGHPONTSPSPASRCQPHTRCENQGLVEAPGTAOSDTTCNPLBPPPMSCMTL 226
DB 167 CVPKAGHPONTSPSPASRCQPHTRCENQGLVEAPGTAOSDTTCNPLBPPPMSCMTL 226
OY 210 --TWLPLVIVFGCLASPAVVLACRYORWKPRLYSLIGOSTLVYRGEPELLVPAPGF 267
DB 210 --TWLPLVIVFGCLASPAVVLACRYORWKPRLYSLIGOSTLVYRGEPELLVPAPGF 267
OY 227 MLAVLPLP--AFLLLATVFSCT-----WKS--HSLCKLGLSKRPFQ-----GEGR 271
DB 227 MLAVLPLP--AFLLLATVFSCT-----WKS--HSLCKLGLSKRPFQ-----GEGR 271
OY 268 NPTTTCFSSSTPSSSPVSIPIY-----ISCDRS--NFGAVAPSSSETAPP----- 310
DB 268 NPTTTCFSSSTPSSSPVSIPIY-----ISCDRS--NFGAVAPSSSETAPP----- 310
OY 272 NPV-----AGSWEPKAPHPFDPLVQPLPISGDVSPVSTGLPAAVLEAGVPOQOS 324
DB 272 NPV-----AGSWEPKAPHPFDPLVQPLPISGDVSPVSTGLPAAVLEAGVPOQOS 324
OY 311 -----HLKAGPLPPEPASTHLCTPGP 332
DB 311 -----HLKAGPLPPEPASTHLCTPGP 332
OY 325 LDLTREPOLEREGSOVAHGTNGIHTGWSNTIGNIYNGPVLGSPGPGDLPATPEP 384
DB 325 LDLTREPOLEREGSOVAHGTNGIHTGWSNTIGNIYNGPVLGSPGPGDLPATPEP 384
OY 333 P-ASTHLCTPGPASTHLCTPVQK 355
DB 333 P-ASTHLCTPGPASTHLCTPVQK 355
OY 385 PYPPEEGDPPPG---LSTPHQE 405
DB 385 PYPPEEGDPPPG---LSTPHQE 405

```

RESULT 6
 GORUN
 nerve growth factor receptor precursor, low affinity (validated) - human
 N/Alternate names: NGF receptor
 C/Species: Homo sapiens (man)
 C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
 C/Accession: A25218; A60204; S21699; I57638
 R/Johnson, D.; Latham, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.;
 Cell 47, 545-554, 1986
 A/Title: Expression and structure of the human NGF receptor.
 A/Reference number: A25218; MUID:87051725; PMID:3022937
 A/Accession: A25218
 A/Molecule type: mRNA

A:Residues: 1-427 <JCH>
A:Cross-references: GB:M14764; NID:G189204; PIDN:AA859544.1; PID:G189205
R:Marano, N.; Diezschold, B.; Barley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A:Reference number: A60204; MUID:87085574; PMID:3025363
A:Accession: A60204
A:Molecule type: protein
A:Residues: 29-31, 'T', '33-42', 'TT', '45-46', 'TX', '50-51', 'XX', '54-56' <MAR>
A:Experimental source: melanoma cell line A875
A>Note: This sequence has been corrected by a note added in proof to follow the nucleot
R:Vasavajhala, F.; Leszyk, J.D.; Lin-Gorke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor rec
A:Reference number: S21689; MUID:92198017; PMID:1372492
A:Accession: S21689
A:Status: preliminary
A:Molecule type: protein
A:Residues: 183-208 <VIS>
R:Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor
A:Reference number: 157638; MUID:89096903; PMID:2850481
A:Accession: 157638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M21621; NID:G189206; PIDN:AA83633.1; PID:G189207
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates w
C:Genetics:
A:Gene: GDB:NGFR
A:Cross-references: GDB:120234; OMIM:162010
A:Map position: 17q21-17q22
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-427/Product: nerve growth factor receptor #status experimental <MAT>
F:32-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NG1>
F:67-108/Domain: NGF receptor repeat homology <NG2>
F:109-187/Domain: NGF receptor repeat homology <NG3>
F:149-189/Domain: NGF receptor repeat homology <NG4>
F:197-248/Region: NGF receptor repeat homology <NG4>
F:197-248/Region: serine/threonine-rich
F:251-273/Domain: transmembrane #status predicted <TM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 236; DB 1; Length 427;
Best Local Similarity 22.9%; Pred. No. 2, 1e-07;
Matches 111; Conservative 62; Mismatches 194; Indels 118; Gaps 22;

7 GLLPLPLVLLADLVAGVGLVPHRGLLEKRRSPCCQKYNHPONSTICCTCKHGT 66
13 PRLILLILLGLSLGAKA-----PPTGLYTH---SGECKKCNIGR 51
67 YLYNDPCPRGDTDRVCAPG--TYTALNHLRLCLSCRCRDEMQLVSPVVDRTVC 125
52 GVAOPC--GANOTVCEPLDVSVDVSAPEPCPCTECVG--LQSNAPCEVADAVC 107
126 GCRKNQRYEWGETFRLCNSLCPNGT-VNIPCOERDPTIC-HGKMFLLKAK-----C 179
108 RC---AYGYQDEFTGRCEACRVCAGSGLVFSCDDKQNTVCBEPDPTYSBEAHNVDP 164
180 ISCHDCK-----NKECKLCPTR-----PSTGKDSODPGTTLVPLVIVFG 220
165 LPTVCEBTERQLRECTRWADAECEI--PGRWITRSTPREGSDSTAPSTOE--PEAPPEQ 221
221 LCISFASVAVLACRQWPKLYSIICGOSTLYKSGBEPLVPAAGFNPPTTITICSSNPS 280
222 DLINSTVAGVVT-----TWGSSQPVVTKGTIDNLIPV-----YCSILIA 260

QY 281 SSPVSIIPPYI-----SCDRSNFGAVASPSSEKAP-----HKAGDILGPPASTHLCT 329
DB 261 AVYGVAVIAYIAFKRMNSCKQKQGANRPVNGQPPPPGKHLKHSQG--ISVDSGLHDOQ 318
QY 330 FGPPASTHLCTPPPPASTHLCTPVQKWEASAPAPDQADAPATLYAVVDGVPSPSWKE 389
DB 319 PHNOTAGCALKGGGGYSSLPAPKREVE-----KLINGSAGDTWRH 361
QY 390 LVRRILGS-SHEIERLEENGRHLREAGYMLAARRRTPREATELLGRVLRDMDLG 448
DB 362 LAGSLGTQPEH-----IDSFTHACPVRLASW--AIQDSXTUDALLAARRIQRAD 412
QY 449 CLENI 453
DB 413 LVEEL 417

RESULT 7
A26431
nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Radake, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shopler, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859; PMID:3027580
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756
R:Merzle, M.; Timusk, T.; Allikmeers, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A:Reference number: PH1229; MUID:93077038; PMID:1446821
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates w
C:Genetics:
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <MAT>
F:30-251/Domain: extracellular #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Region: serine/threonine-rich
F:252-273/Domain: transmembrane #status predicted <TM>
F:274-425/Domain: intracellular #status predicted <INT>
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.7%; Score 227.5; DB 1; Length 425;
Best Local Similarity 23.4%; Pred. No. 6, 8e-07;
Matches 107; Conservative 59; Mismatches 169; Indels 123; Gaps 24;

44 CPQCKYNHPONSTICCTCKHGTLYNDPCPRGDTDRVCAPG--TYTALNHLRLCLSC 102
DB 33 CSTGLYTH---SGECKACNIGBGVAOPC--GANOTVCEPLDVTTSVDVSAPEPCAPC 87
QY 103 SRCRDEMQLVSPVVDRTVCRCRKNQRYEWGETFRLCNSLCPNGT-VNIPCOER 161
DB 88 TECIG--LQSNAPCEVADAVCAVGYOD--EETG-HCEACSVCEVSGLVFSCDDX 142
QY 162 QDTIC-HGKMFLLKAK-----CISCHDCKNKECKLCPTRPSTGKDSOD-PGTTVLLPL 215

```

Db      143 QNTVEBECGEGTVSDANVDPCLPCTVEDTE-RQLRRECTPWADAECEITG----- 194
Qy      216 VVFGCLCLASFPASVVLACRYQWKPKLYSIICQSTLVKEGPEL-----LVPAQFNP 270
Db      195 -----RWIPRSTPEGSDSTAPSTOEPEVPPEODLVPSTVADAV 233
Qy      271 TTICFSTP-----SSPVSIPIYI-----SCDRNPGAVASPSSE 306
Db      234 TTVKSSSGCVVTRGTTDNLIPIVYCSILAAVVGVLAVYIAFKMNSCKQKQGANRPVNO 293
Qy      307 TAPP-----HLKAGPILPGRPASTHLCTPBPASTHLCTPBPAA-----STHLCTPVQW 356
Db      294 TPPEGEKIHSDG--ISVDSGLH-----DOCHTQVASGALKGDGNLVSSLPLTKR 345
Qy      357 EMSASAPDQGLADADPATIYAVDGVPPSRMKELVRLGLS-EHEIERLELENGHLEBA 415
Db      346 E-----EVERKLNGD-----TWRLHAGELGYOPEH-----IDSFTHACP 380
Qy      416 QYSMLAARRRTRPREATELGLRVLRMDLGLCENI 453
Db      381 VRALLASWCAQD---SATIDALLALRLRQRADYBSL 415

```

RESULT 8

nerve growth factor receptor, low affinity precursor - chicken

N.Alternate names: NGF receptor

C.Species: Gallus gallus (chicken)

C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C.Accession: JN0006; A60504

R.Larsge, T.H.; Weiskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid

Neuron 2, 1123-1134, 1989

A.Title: Structure and developmental expression of the nerve growth factor receptor in t

A.Reference number: JN0006; MUID:90166579; PMID:2560385

A.Accession: JN0006

A.Molecule type: mRNA

A.Residues: 1-416 <LAR>

A.Experimental source: embryonic chick brain

R.Heuer, J.G.; Falcami-Nainie, S.; Wheeler, E.F.; Bothwell, M.

Dev. Biol. 137, 287-304, 1990

A.Title: Structure and developmental expression of the chicken NGF receptor.

A.Reference number: A60504; MUID:90152140; PMID:2154393

A.Accession: A60504

A.Molecule type: preliminary; not compared with conceptual translation

A.Residues: 21-35, 'Y', 37-172, 'K', 174-215, 'S', 277-395, 'R', 397-416 <HEU>

C.Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma

C.Comment: This cytosolic-rich region of the extracellular domain may form part or all of

C.Comment: This protein is thought to form a high-affinity receptor when it associates w

C.Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t

F.1-20/Domain: signal sequence #status predicted <SIG>

F.21-416/Product: nerve growth factor receptor #status predicted <MNT>

F.21-235/Domain: extracellular #status predicted <EXT>

F.24-57/Domain: NGF receptor repeat homology <NG1>

F.59-100/Domain: NGF receptor repeat homology <NG2>

F.101-119/Domain: NGF receptor repeat homology <NG3>

F.141-181/Domain: NGF receptor repeat homology <NG4>

F.189-237/Region: serine/threonine-rich

F.240-251/Domain: transmembrane #status predicted <MEM>

F.262-416/Domain: intracellular #status predicted <INT>

F.52/Binding site: carbohydrate (Asn) (covalenc) #status predicted

Query Match 8.5% Score 220; DB 1: Length 416;

Best Local Similarity 23.3% Pred. No. 1.9e-06;

Matches 116; Conservative 46; Mismatches 168; Indels 168; Gaps 25;

Qy 6 VPGLLPVLVLPALLADVYPAGVQGLVPRPGDLEKRESFPCQKYNHPQNSTICTCKGKG 65

Db 5 VFLVLLVLL-----PAG-----PTWGSKEK-----CLTKMT---TSECCCKACNLG 42

Qy 66 TYLVNDGCGPRDIDDCVCAPE-TYTALENHLRLRCLSCSRCDENFOVEISPCVVDRTV 124

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Db      43 EGVQPPC--GVNOYVCEPCLDSTVTSSTVSAITBPKPCTQCVG--LHSMAPCVESDDAV 98
Qy      125 QGCRKNQRYEYWGTEGFRCLNCSLCPNG-TVINPQOERODTIC-HCHMGFLPKGAK----- 178
Db      99 CRC--AVGYQDELSSGCKECSICEVQFGMLPFCRDSQDITVCECEPGCTGSDANFVDP 155
Qy      179 CISCIDCK-----NKECEKLCR-----TRPSTKDSODPCT-----T 210
Db      156 CLPCTTCENENVMWKECTASTDABCRDLHPRTWTTTSLASDSBPEPTTRDPFTEGMAT 215
Qy      211 VLLPLVYIFGLCLASFPASVVLACRYQWKPKLYSIICQSTLVKEGPELVLPAQFNP 270
Db      216 TLADIIVT-----TVKSSGCVVTRGTTDNLIPIV----- 243
Qy      271 TTICFSSSTPSSPVSIPIYI-----SCDRNPGAVASPSSETAP-----HLKAGPILP 319
Db      244 -----YCSILAAVVGVLAVYIAFKMNSCKQKQGANRPVNOQPSPEGEKIHSDGISVD 299
Qy      320 GPAPASTHLCTPBPASTHLCTPBPASTHLCTPVQKWEASAPADQGLADADPATIYAVV 379
Db      300 -----SGLHDOQPPNOQ---TQGP-----APKGDGLVA-- 326
Qy      380 DGVPPSR-----WKELVRLGLSEHIERLELENGRHLREAOYGMLAAR 424
Db      327 -SLPPSKQEBVEKLLSSAERTWQLAGELQYKEDLIDCFIRE-----ESPAALADW- 379
Qy      425 RRTPREATELGLRVLR 442
Db      380 --SAKETATIDALLVALR 395

```

RESULT 9

death receptor-6 - chicken

C.Species: Gallus gallus (chicken)

C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C.Accession: JG7705

R.Bridgman, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A.Title: Conservation of death receptor-6 in avian and placine vertebrates.

A.Reference number: JG7705; MUID:21308433; PMID:11414698

A.Accession: JG7705

A.Molecule type: mRNA

A.Residues: 1-651 <BRI>

A.Cross-References: GB:AP349808

C.Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs

C.Comment: to a class of receptors that activate a cell death and/or survival signaling cascade.

C.Keywords: dr-6

F.1-21/Domain: signal sequence #status predicted <SIG>

F.52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>

F.332-350/Domain: transmembrane #status predicted <TM>

F.410-475/Domain: death domain #status predicted <DED>

F.551-651/Region: conserved cytoplasmic #status predicted

Query Match 7.7% Score 199.5; DB 2: Length 651;

Best Local Similarity 22.9% Pred. No. 5.3e-05;

Matches 125; Conservative 57; Mismatches 217; Indels 147; Gaps 30;

Qy 10 LPLPLVLPALV-----ADVPRAGVQGLVPRPGDLEKRESFPCQKYNH-----PQNSTICTCK 62

Db 5 VLAVALPLVFLGTRADQPKLT-----EQNAVSLPAGKYLHIDRAKTNOELICDKC 55

Qy 63 HKGTLYLVNDGCGPRDIDDCVCAPE-TYTALENHLRLRCLSCSR-CDENFOVEISPCVV 119

Db 56 PACTYVSKHCT--KSTLRKCSPPCDGTPTKHENGIERCHPRKRPC--ELPMIEKTHCTA 110

Qy 120 DRDTVQCGCRKNQRYEYWGTEGFRCLNCSLCPNG-TVINPQOERODTIC-HCHMGFL 173

Db 111 LTIRECTCLSGTF-----QINDTCVPYTVCPVGVGVRKKGKTEDEVDRCKPCLRGTSFDPV 165

A42086
CD30 antigen precursor - human
M:Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C:Accession: A42086
R:Durkop, H.; Latzer, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.
Cell 68, 421-427, 1992
A:Title: Molecular cloning and expression of a new member of the nerve growth factor rec
A:Reference number: A42086; MUID:92154659; PMID:1310894
A:Accession: A42086
A:Molecule type: mRNA
A:Residues: 1-595 <DUF>
A:Cross-references: GB:M83554; NID:9180095; PIDN:AAA51947.1; PID:9180096
A:Experimental source: HUT-102 cell line
A:Note: Sequence extracted from NCBI Backbone (NCBIN:82088, NCBI:82090)
C:Genetics:
A:Gene: GDB:CD30; DIS166
A:Cross-references: GDB:131547; OMIM:153243
A:Map position: 1p36-1p36
C:Superfamily: NGF receptor repeat homology
C:Keywords: glycoprotein; growth factor receptor; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-383/Domain: extracellular #status predicted <EXT>
F:384-407/Domain: transmembrane #status predicted <TM>
F:408-595/Domain: intracellular #status predicted <CYT>
F:101,276/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 7.4%; Score 193; DB 2; Length 595;
Best Local Similarity 24.6%; Pred. No. 0.0012;
Matches 101; Conservative 42; Mismatches 166; Indels 102; Gaps 24;

Oy 41 ESPCGQKYNHQNSTI--CCTKCHKGYLYNDGCPGRDPCR-VCAFGTYTALENLR 97
Db 26 EDTC-HGPHSHYDAVRCCTCRPMGLFPTQC--PGRPTDCKKQSPDYTL--DDAD 79
Oy 98 RCLSCSRC-RDEMFQVEISPCVDRDTVCGRKNQRYEWG-ETGPRCLNCSLCPNG-TV 154
Db 80 RCTACVTCSSRDL-VKTPCAMNNSRYCECRPGMFCSTAVNSCARCFPHSVCAQMITV 137
Oy 155 NIPQERDPTTICH-CHMFPFLKGAACISCHDCKNEC-----EKLCPTRPST----- 200
Db 138 KPGTAQKNTVCEPASPV---SPACASPENCKEPPSSGTTPOAKPTPVSPATSSATMPV 194
Oy 201 -----GKDSQDPETTVLLVIVFGICLASFASVLAQRYQ 236
Db 195 RGTRIAQDAASKLTRADSPSSVGRPSDPELSTQPCPEGSDC-----RK 242
Oy 237 RMKRLVYSIICQGST-LVKEGPELLVPAP-GFNPTT-----ICFSSTPSSSPVISP 287
Db 243 QCEPDYVDEAGRCACVSCSRDLVEKTPCAMNNSRYCECRPGMFCSTAVNSCARCV- 301
Oy 288 PYISCDNRNFGAVASPSSETAPRH-KAGPILPGPPASTHL-CTPGP-----PASTHLCT 340
Db 302 PYPIC-----AAETVTKQDAEEDTTFEAPPLCTOPDCNTPENGAPAST----- 348
Oy 341 PGPPASTHLCTPVQKWEASAPADQADADPATLVAVDVQPPSRMELV 391
Db 349 -SPQSLVLDVDSQASKTLPIPTSAVALS-----STGKPVLDAGPVLEWILV 394

RESULT 12
JC2395
Fas antigen precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C:Accession: JC2395; PC2246
R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat live
A:Reference number: JC2395; MUID:94128114; PMID:7507668
A:Accession: JC2395
A:Molecule type: mRNA

A:Residues: 1-324 <KIM>
A:Cross-references: DBJ:D26112; NID:9468486; PIDN:BA05108.1; PID:d1005650; PID:9468487
A:Experimental source: thymus
A:Accession: PC2246
A:Molecule type: mRNA
A:Residues: 1-62, 'RFT' <K12>
A:Cross-references: DBJ:D26113; NID:9468488; PIDN:BA05109.1; PID:d1005651; PID:9468489
A:Experimental source: liver
C:Genetics:
A:introns: 62/1
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-324/Product: Fas antigen #status predicted <MAT>
F:44-79/Domain: NGF receptor repeat homology <NGF>
F:81-124/Domain: NGF receptor repeat homology <NG4>
F:171-188/Domain: transmembrane #status predicted <TM>

Query Match 7.0%; Score 181.5; DB 2; Length 324;
Best Local Similarity 23.5%; Pred. No. 0.00034;
Matches 71; Conservative 39; Mismatches 107; Indels 85; Gaps 13;

Oy 10 LPLVLPALADVYPAGVGL---VPHGDLKESPPQCKYHNPONSTICCTKCHKGT 66
Db 7 VLPLVLAGPELVNMGCDSTFEGLELKRSTRETDNNSSEGLY---QVGPCCOCPGCE 63
Oy 67 YLVNDCPGRGDTDCRVACAP-TYTALENHLRLCLSCSRCHDEMFOVEI-SPCVDRDTV 124
Db 64 RKVDDCTTSGAPFCHPCTEGEBEYDRKHYSDKRCRAFC-DEGHGLEVEFTNCRQTQTK 122
Oy 125 CGCRKNQRYEHWGTRGRCCLMCSLCPNQTIVIPQERDPTICHMGMFLGACISCHD 184
Db 123 CRCKENFY-----CNASLCDH-----CYHCTS 144
Oy 185 CKNKECEKLCPTRPSTGKDSQDPETTVLLPLVIVFGICLASFASVLAQRYQWKPKLYS 244
Db 145 CGLBDILKPC-TRNSNTRCKKQSSNYKLWLLPLGLAI---LVFYIKRYRKQP----- 196
Oy 245 IICGOSTLVKEGPELVAPGFPPTTTCSSPSS-SPVSIPTPYI-----SCDRS 295
Db 197 -----GDPESGIPSP-----ESVPMNVSDVNLKMYIWRTRKMKICPAK 235
Oy 296 NF 297
Db 236 KF 237

RESULT 13
B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus, Shope fibroma virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: B43692
R:Upton, C.; Delange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A:Reference number: A43692; MUID:87321103; PMID:2820128
A:Accession: B43692
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:Cross-references: GB:M17433
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 7.0%; Score 181.5; DB 2; Length 325;
Best Local Similarity 29.6%; Pred. No. 0.00034;
Matches 58; Conservative 16; Mismatches 81; Indels 41; Gaps 12;

Oy 14 VLPLADVYPAGVGLVPHGDLKESPPQCKYHNPONSTICCTKCHKGYLYNDP 73
Db 4 LIALVLCVVVYVYGD--VPY-----SSNQGKCGGHDY---EKDGLCCASCHGPFASRLC- 53

QY 74 GPGADTDRCVCAFGTYTALLENHLRRCLSC-SRCDREMFQVEISPCVVDRTDVGCRKNQY 132
 DB 54 GPGSTVSPCEDGFTLSTHAPACVSCRGCTGHL--SESQPCDRTHDRVCNCTGNY 111
 QY 133 REYMGCTFRCLNGLCNGTATNIPQERQDPTICHCHNGFLKAKCSCHD-CNKKECE 191
 DB 112 CLKKGNG-----CRICAPQT-----KCPAGVGS-----HTRADDTLCE 147
 QY 192 KLCEPTRPSTGKDSQDP 207
 DB 148 K-CP--PHTYSDSLSP 160

RESULT 14

T2 protein - myxoma virus (strain Lausanne)
 C/Species: myxoma virus
 C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
 C/Accession: A40566
 R/Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
 Virology 184, 370-382, 1991
 A/Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor
 A/Reference number: A40566; MUID:91335768; PMID:1651597
 A/Accession: A40566
 A/Molecule type: DNA
 A/Residues: 1-326 <UP>
 A/Cross-references: GB:M5181; GB:M37976; NID:G332309; PID:AAA6632.1; PID:G332310
 C/Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 C/Keywords: glycoprotein
 F/64-105/Domain: NGF receptor repeat homology <NG2>
 F/106-147/Domain: NGF receptor repeat homology <NG3>
 F/166-181,205,238/binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 6.9%; Score 180; DB 1; Length 336;
 Best Local Similarity 35.5%; Pred. No. 0.00042;
 Matches 50; Conservative 11; Mismatches 64; Indels 16; Gaps 7;
 QY 14 VLPALADVPAVGVGLVPHRDLKRESPPQGRKNHPONSTICTCKHKGTYLYNDCP 73
 DB 6 LLNAVACVYGGG-----APYGADRGK-----CRGNKY-----EKDGLCTSCPPGSAVRNC- 53
 QY 74 GPGADTDRCVCAFGTYTALLENHLRRCLSC-SRCDREMFQVEISPCVVDRTDVGCRKNQY 132
 DB 54 GPGSTVSPCEDGFTLSTHAPACVSCRGCTGHL--SESQPCDRTHDRVCNCTGNY 111
 QY 133 REYMGCTFR-CLNGLCPNG 152
 DB 112 CLKKGNGCRICAPRTKCPAG 132

RESULT 15

B38634
 Tumor necrosis factor receptor type 2 precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C/Accession: B38634; A40254; S54816
 R/Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A/Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
 A/Reference number: A38634; MUID:91187885; PMID:1849278
 A/Accession: B38634
 A/Molecule type: mRNA
 A/Residues: 1-474 <LEW>
 A/Cross-references: GB:M60469; NID:G199827; PID:AAA39752.1; PID:G199828
 R/Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
 Mol. Cell. Biol. 11, 3020-3026, 1991
 A/Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
 A/Reference number: A40254; MUID:91246168; PMID:1645445
 A/Accession: A40254
 A/Molecule type: mRNA
 A/Residues: 1-474 <GOO>
 A/Cross-references: GB:M60469; NID:G199827; PID:AAA39752.1; PID:G199828

R/Kisnerghis, M.; Fellous, R.; Feldmann, M.; Chernajovsky, Y.
 submitted to the EMBL Data Library, May 1995
 A/Description: Characterization of the promoter region of the murine p75-TNF receptor.
 A/Reference number: S54816
 A/Accession: S54816
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-72 <KIS>
 A/Cross-references: EMBL:X87128; NID:G809043; PID:CAA60618.1; PID:G809044
 C/Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C/Keywords: cytokine receptor; transmembrane protein
 F/1-22/Domain: signal sequence, #status predicted <SIG>
 F/23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F/40-77/Domain: NGF receptor repeat homology <NG1>
 F/79-120/Domain: NGF receptor repeat homology <NG2>
 F/166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 6.9%; Score 178.5; DB 2; Length 474;
 Best Local Similarity 23.1%; Pred. No. 0.00075;
 Matches 80; Conservative 36; Mismatches 138; Indels 93; Gaps 16;
 QY 32 PHPDLEKRESPPQGRKNHPONSTICTCKHKGTYLYNDCRGGRDTRDRCVCAFGTYTA 91
 DB 34 PEPG-----YECISQSYIDRKAQWCCAKCPQGVYHFC-NKTSPTVCADCEASMTTQ 86
 QY 92 LENHLRRCLSC-SRCDREMFQVEISPCVVDRTDVGCRKNQYREYMGCTGF--RCLNCSL 148
 DB 87 VMNQFRCLSSSSCTTD--QVEIRACIKQGNRCACBAAGYCALKTHSSGCRQCMRLSK 144
 QY 149 C-----PQGTATNIPQERQDPTICHCHNGFLKAKCSCHDCKNKECKLCEPTR 197
 DB 145 CGPFGVAASRAAPNGNV-----LC-----KAC--A 167
 QY 198 PSTGKDSQDPRTTLLPLVIVFGLCLASFASVVLACRYGRKPKLYSLICQSTLVYEGE 257
 DB 168 PGTISDTTS-STDCRPHRLCSILALPQNASSTDAVCAPE--SPTLSAI--PRTLYVSQPS 222
 QY 258 PEL-----LVPAQFNPTTITCFSSSTP-----SSPVSIPPIYISCDPSNFG-----A 299
 DB 223 PTRSQPLDQBERGPGTQTSILTSLSSTPIIBSTGCGSLPIGLIVGTSLGLMLGLVNC 282
 QY 300 VASPSSETAPPHLKAGPILPEPP-----ASTHLCTPGPPAST 336
 DB 283 IILVQRKKKPSCLORDAKVPHVPEKSDAVGLEQHLTLTAPSSSS 329

Search completed: September 13, 2003, 07:06:06
 Job time : 22 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2003, 06:56:04 ; Search time 17 Seconds

(without alignments)
1302.916 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603
Sequence: 1 MGLPTVGGLLPLVLPALLA.....NIEFALGAMRLASEPRLLW 471

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2603	100.0	471 1	TR1A_BOVIN
2	1750	67.2	461 1	TR1A_PIG
3	1517	58.3	455 1	TR1A_HUMAN
4	1338.5	51.4	461 1	TR1A_RAT
5	1319	50.7	454 1	TR1A_MOUSE
6	387.5	14.9	417 1	TR25_HUMAN
7	271.5	10.4	440 1	TR10B_HUMAN
8	257	9.9	435 1	TRR3_HUMAN
9	247	9.5	415 1	TRR3_MOUSE
10	236	9.1	427 1	TR16_HUMAN
11	227.5	8.7	425 1	TR16_RAT
12	221.5	8.5	417 1	TR16_MOUSE
13	220	8.5	416 1	TR16_CHICK
14	199	7.6	461 1	TR1B_HUMAN
15	196	7.5	176 1	TR23_MOUSE
16	195	7.5	655 1	TR21_HUMAN
17	195	7.5	655 1	TR21_MOUSE
18	194.5	7.5	180 1	TRR2_MOUSE
19	193	7.4	595 1	TRR8_HUMAN
20	191.5	7.4	381 1	TR10B_MOUSE
21	185	7.1	468 1	TRR6_RAT
22	181.5	7.0	324 1	TRR6_MOUSE
23	181.5	7.0	325 1	TRR6_PIG
24	180	6.9	326 1	TRR6_BOVIN
25	178.5	6.9	474 1	TRR6_MOUSE
26	171.5	6.6	259 1	TRR6_MOUSE
27	171.5	6.6	283 1	TRR6_MOUSE
28	169	6.5	3718 1	TRR6_MOUSE
29	168.5	6.5	289 1	TRR6_MOUSE
30	167	6.4	332 1	TRR6_PIG
31	167	6.4	323 1	TRR6_MOUSE
32	166	6.4	351 1	TRR6_MOUSE
33	166	6.4	401 1	TRR6_MOUSE

34	163.5	6.3	349 1	CRMB_CAMPS
35	163.5	6.3	349 1	CRMB_VARV
36	162	6.2	386 1	TR10B_HUMAN
37	161	6.2	327 1	TRR6_MOUSE
38	160.5	6.2	300 1	TRR6_HUMAN
39	160.5	6.2	1696 1	PKCS_BRACL
40	160	6.1	401 1	TR1B_MOUSE
41	158	6.1	824 1	AD08_HUMAN
42	155.5	6.0	269 1	TRR5_BOVIN
43	155	6.0	1877 1	PKCS_MOUSE
44	154.5	5.9	870 1	SRG2_HUMAN
45	153.5	5.9	625 1	TR11_MOUSE

ALIGNMENTS

RESULT 1

ID	TR1A_BOVIN	STANDARD	PRG	471 AA.
AC	019131;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)			
DE	(TNF-R1) (TNF-R1) (p55).			
GN	TNFRSF1A OR TNFR1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
NCBI	TaxID=9913;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RA	MEDLINE=96273505; PubMed=9613449;			
RT	Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;			
RT	"Cloning and sequencing of cDNA encoding bovine tumor necrosis factor (TNF)-receptor I."			
RL	Vet. Immunol. Immunopathol. 61:379-385(1998).			
CC	-1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/Lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis (by similarity).			
CC	-1- SUBUNIT: Binding of TNF to the extracellular domain leads to homotrimerization. The aggregated death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFs, RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling.			
CC	Binds Bcl2 (by similarity).			
CC	-1- SUBCELLULAR LOCATION: Type 1 membrane protein.			
CC	-1- SIMILARITY: Contains 4 TNFR-Cys repeats.			
CC	-1- SIMILARITY: Contains 1 death domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_email_to_license@sib.ch).			
CC	EMBL: U90937; AAB65143.1; .			
CC	HSSP: P19438; 1TRR.			
CC	InterPro: IPR000489; Death.			
CC	InterPro: IPR001368; TNFR_C6.			
CC	Pfam: PF00531; death.1.			
CC	Pfam: PF00020; TNFR_C6; 3.			
CC	SMART; SM00005; DEATH; 1.			

DR SMART; SMO0208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00505; TNFR_NGFR_2; 3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 471
 FT DOMAIN 22 210
 FT TRANSMEM 211 233
 FT DOMAIN 234 471
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 195
 FT DOMAIN 340 360
 FT DOMAIN 360 360
 FT DOMAIN 372 457
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 194
 FT DISULFID 185 190
 FT CAROAMD 54 54
 FT CAROAMD 145 145
 FT CAROAMD 151 151
 SO SEQUENCE 471 AA; 51367 MW; 5243EF51ADF8B1C4 CRC64;

Query Match 100.0%; Score 2603; DB 1; Length 471;
 Best Local Similarity 100.0%; Pred. No. 4,3-159;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLPVPGLLLPLVLPALLADYVPAGVGVHPGDLERESPCCQKYNHNPONSTICT 60
 DB 1 MGLPVPGLLLPLVLPALLADYVPAGVGVHPGDLERESPCCQKYNHNPONSTICT 60
 QY 61 KCHKSTLYNDPCPGGRDTCRCVCAPTGTALLENLRCLSCGRSDMPQVEISPCVVD 120
 DB 61 KCHKSTLYNDPCPGGRDTCRCVCAPTGTALLENLRCLSCGRSDMPQVEISPCVVD 120
 QY 121 RDTVCGCKKNOYREYWGEGFRCNLCSLCPNGTVNI PCQERODTI CHCHMGFPLKAGCT 180
 DB 121 RDTVCGCKKNOYREYWGEGFRCNLCSLCPNGTVNI PCQERODTI CHCHMGFPLKAGCT 180
 QY 181 SCHDCKNKECEKLCPTPSTGKSDPGTTLVPLVIVFGCLASFASVVLACRYQWKP 240
 DB 181 SCHDCKNKECEKLCPTPSTGKSDPGTTLVPLVIVFGCLASFASVVLACRYQWKP 240
 QY 241 KLYSIICQSTLYKGEPELLVPAGFNPTTICFSSSTPSSSPVSIPIYISCDRSNFGAV 300
 DB 241 KLYSIICQSTLYKGEPELLVPAGFNPTTICFSSSTPSSSPVSIPIYISCDRSNFGAV 300
 QY 301 ASPSEETAPPHLKACPIIPGPASTHLCCTPGPASTHLCCTPGPASTHLCCTPVQWMSA 360
 DB 301 ASPSEETAPPHLKACPIIPGPASTHLCCTPGPASTHLCCTPGPASTHLCCTPVQWMSA 360
 QY 361 PSAPQCLADADPATLYAVVDGVPSPRMKELVRIGLSHETIRLENGRHLREAOYMTL 420
 DB 361 PSAPQCLADADPATLYAVVDGVPSPRMKELVRIGLSHETIRLENGRHLREAOYMTL 420
 QY 421 AAMRRRTRENTLELGRVLRDMDLGCLENIEBAGLAARLASEPRLW 471
 DB 421 AAMRRRTRENTLELGRVLRDMDLGCLENIEBAGLAARLASEPRLW 471

RESULT 2
 TRIA_PIG

ID TRIA_PIG STANDARD; PRT; 461 AA.
 AC PS0555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 DE (TNF-R1) (TNF-R1) (p55).
 GN TNFRSF1A OR TNFR1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleostomi; Cetartiodactyla; Suidae; Sus.
 ON NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Kidney;
 RC MEDLINE=96011645; Pubmed=7590278;
 RA Suter B., Pauli U.H.;
 RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor";
 RU Gene 163:263-266(1995).
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (apoptate-specific cysteine proteases) mediating apoptosis (By similarity).
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to homotrimerization. The aggregated death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFs, RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling.
 CC Blinde Baga (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; U19594; AAC48499.1; .
 DR PIR; JC4302; JC4302.
 DR HSP; P19438; TNFR.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00531; death_1.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR SMART; SMO0005; DEATH; 1.
 DR SMART; SMO0208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00505; TNFR_NGFR_2; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 461
 FT DOMAIN 22 210
 FT TRANSMEM 211 233
 FT DOMAIN 234 461
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 195
 FT DOMAIN 340 350
 FT DOMAIN 362 447
 FT DISULFID 44 58
 FT DISULFID 59 72

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FT DISULFID 62 81 BY SIMILARITY.
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FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 194 BY SIMILARITY.
FT DISULFID 185 190 BY SIMILARITY.
FT CARBOHYD 54 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

Query Match 67.2%; Score 1750; DB 1; Length 461;
Best Local Similarity 70.2%; Pred. No. 9.7e-105;
Matches 339; Conservative 24; Mismatches 84; Indels 36; Gaps 5;

QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGKYNHPNSTICT 60
DB 1 MGLSTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGKYNHPNSTICT 60
QY 61 KCHKGTLYNDPCPGPDTDCRCVCAPTVYALENHRLRCLSCSRGDMFQVEISPCVVD 120
DB 61 KCHKGTLYNDPCPGPDTDCRCVCAPTVYALENHRLRCLSCSRGDMFQVEISPCVVD 120
QY 121 RDTVCGCKXKQYREYWGTFGRCLNCSLCRNGTANNIPCEKODPTCHGMGFPLKAKCI 180
DB 121 RDTVCGCKXKQYREYWGTFGRCLNCSLCRNGTANNIPCEKODPTCHGMGFPLKAKCI 180
QY 181 SCHDCKNKECEKLCPTRPSTGKSDQDPGTVLLPLVYFGCLASFASVAVLACRYQRMKP 240
DB 181 SCHDCKNKECEKLCPTRPSTGKSDQDPGTVLLPLVYFGCLASFASVAVLACRYQRMKP 240
QY 181 SCVCKNADCKNLCNCPATSETENDPDGTITVLLPLVIFGLCLAFPLVGLACRYQRMKP 240
DB 181 SCVCKNADCKNLCNCPATSETENDPDGTITVLLPLVIFGLCLAFPLVGLACRYQRMKP 240
QY 241 KLVYIIGQSTLVKGEDELLVPAEGNPPTTI-----CRSTPSSSPVSIPIYI 290
DB 241 KLVYIIGQSTLVKGEDELLVPAEGNPPTTI-----CRSTPSSSPVSIPIYI 290
QY 241 KLVYIIGQSTLVKGEDELLVPAEGNPPTTI-----CRSTPSSSPVSIPIYI 290
DB 241 KLVYIIGQSTLVKGEDELLVPAEGNPPTTI-----CRSTPSSSPVSIPIYI 290
QY 291 SCDSNPFCAVSPSESTAPPHLKAGPLIPGPPASHLCTPGPPASHLCTGPPASHLCT 350
DB 291 SCDSNPFCAVSPSESTAPPHLKAGPLIPGPPASHLCTPGPPASHLCTGPPASHLCT 350
QY 301 PCDSNSNI-KVTSPPKELAPPGAGPLPMPAS-----TVP----- 337
DB 301 PCDSNSNI-KVTSPPKELAPPGAGPLPMPAS-----TVP----- 337
QY 351 TPVOKWEA---SAPSAPDQADADPATLYAVDGPSPSKMELVRLGLSEHEIRLELE 407
DB 351 TPVOKWEA---SAPSAPDQADADPATLYAVDGPSPSKMELVRLGLSEHEIRLELE 407
QY 338 TPLKMGKSAISAPAPQADADPATLYAVDGPSPSKMELVRLGLSEHEIRLELE 397
DB 338 TPLKMGKSAISAPAPQADADPATLYAVDGPSPSKMELVRLGLSEHEIRLELE 397
QY 408 NGRHLREAOYSLAMARRRTPREATELLEGRVLRDMDLGCLNIBBALGGAARLASEP 467
DB 408 NGRHLREAOYSLAMARRRTPREATELLEGRVLRDMDLGCLNIBBALGGAARLASEP 467
QY 398 NGRCLREAOYSLAMARRRTPREATELLEGRVLRDMDLGCLNIBBALGGAARLASEP 457
DB 398 NGRCLREAOYSLAMARRRTPREATELLEGRVLRDMDLGCLNIBBALGGAARLASEP 457
QY 468 RLL 470
DB 468 RLL 470
QY 458 HLL 460
DB 458 HLL 460

RESULT 3
TRIA HUMAN STANDARD; PRT; 455 AA.
AC TRIA438;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55) (CD120a) (Contains: Tumor necrosis factor
DE binding protein 1 (TBP1)).
GN TNFRSF1A OR TNFR1 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxId=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90235285; PubMed=2158863;
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;
RT "Molecular cloning and expression of a receptor for human tumor
RT necrosis factor."
RL Cell 61:361-370(1990).
RP SEQUENCE FROM N.A.
RX MEDLINE=90235284; PubMed=2158862;
RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA Tabuchi H., Lesslauer W.;
RT "Molecular cloning and expression of the human 55 kd tumor necrosis
RT factor receptor."
RL Cell 61:351-359(1990).
RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53, 110-124 AND 199-201.
RX MEDLINE=9106021; PubMed=1698610;
RA Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zhang R.,
RA Aderka D., Holtmann H., Wallach D.;
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT for the type I TNF-R, cloned using amino acid sequence data of its
RT soluble form, encodes both the cell surface and a soluble form of the
RT receptor."
RL EMBO J. 9:3269-3278(1990).
RP SEQUENCE FROM N.A.
RX MEDLINE=9109884; PubMed=1702293;
RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein."
RL DNA Cell Biol. 9:705-715(1990).
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RC MEDLINE=91017509; PubMed=2170974;
RA Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT expression of recombinant soluble TNF-binding protein."
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RP SEQUENCE FROM N.A.
RX MEDLINE=92250049; PubMed=1315717;
RA Fuchs P., Strehl S., Dwozrak M., Himmler A., Ambros P.F.;
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT localization to chromosome 12p13."
RL Genomics 13:219-224(1992).
RP SEQUENCE FROM N.A.
RX MEDLINE=922386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh F.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villation D.K., Muzny K.C., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Shevchenko Y., Boulfard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywiecki M.I., Skalska U., Smallus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [9]
 RP SEQUENCE OF 41-45.
 RX MEDLINE=90110215; PubMed=2153336;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 RT urine. Evidence for immunological cross-reactivity with cell surface
 RT tumor necrosis factor receptors.";
 RL J. Biol. Chem. 265:1531-1536 (1990).
 RN [10]
 RP INTERACTION WITH BAG4.
 RX MEDLINE=99115917; PubMed=9915703;
 RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
 RT "Prevention of constitutive TNF receptor 1 signaling by silencer of
 RT death domains.";
 RL Science 283:543-546 (1999).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
 RX MEDLINE=93258809; PubMed=8387891;
 RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
 RA Broger C., Loetscher H., Lesslauer W.;
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
 RT beta complex: implications for TNF receptor activation.";
 RL Cell 73:431-445 (1993).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
 RX MEDLINE=97094982; PubMed=8939750;
 RA Nalesmith J.H., Devine T.O., Khono H., Sprang S.R.;
 RT "Structure of the extracellular domain of the type I tumor necrosis
 RT factor receptor.";
 RL Structure 4:1251-1262 (1996).
 RN [13]
 RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
 RX MEDLINE=99213501; PubMed=10199409;
 RA McCormick M.F., Akentjevich I., Galon J., McCormick E.M.,
 RA Ogunkolade B.W., Centola M., Mansfield E., Gadiña M., Karanko L.,
 RA Peterson T., McCarter J., Frucht D.M., Aringer M., Torosyan Y.,
 RA Teppo A.-M., Wilson M., Karaazalan H.M., Wan Y., Todd I., Wood G.,
 RA Schlimen R., Kumaraswami T.R., Cooper S.M., Vella J.P., Amos C.I.,
 RA Mulvey J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,
 RA Hilman G.A., O'Shea J., Kaestner D.L.;
 RT "Germline mutations in the extracellular domains of the 55 kDa TNF
 RT receptor, TNFR1, define a family of dominantly inherited
 RT autoinflammatory syndromes.";
 RL Cell 97:133-144 (1999).
 RN [14]
 RP FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
 CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis. Contributes to
 CC the induction of noncytotoxic TNF effects including anti-viral
 CC state and activation of the acid sphingomyelinase.
 CC -1 SUBUNIT: Binding of TNF to the extracellular domain leads to
 CC homotrimerization. The aggregated death domains provide a novel
 CC molecular interface that interacts specifically with the death
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
 CC RIP and possibly FADD, are recruited to the complex by their
 CC association with TRADD. This complex activates at least two
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
 CC Binds BAG4.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein and secreted.
 CC -1 DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
 CC -1 PTM: The soluble form is produced from the membrane form by
 CC proteolytic processing.
 CC -1 DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant

CC familial hibernian fever (FHF), a disease characterized by
 CC recurrent fever, abdominal pain, localized tender skin lesions and
 CC myalgia.
 CC -1 SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1 SIMILARITY: Contains 1 death domain.
 CC -1 DATABASE: NAME=PROV; NOTE=CD guide CD120a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".
 CC -----
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 CC DR EMBL; M33294; AAA03210.1; -;
 CC DR EMBL; M58286; AAA36753.1; -;
 CC DR EMBL; M63121; AAA36754.1; -;
 CC DR EMBL; M75866; AAA61201.1; -;
 CC DR EMBL; M75864; AAA61201.1; JOINED.
 CC DR EMBL; M75865; AAA61201.1; JOINED.
 CC DR EMBL; M60275; AAA36756.1; -;
 CC DR EMBL; A21522; CAAB1558.1; -;
 CC DR EMBL; A131997; AAM77802.1; -;
 CC DR EMBL; BC010140; AAM77802.1; -;
 CC DR PIR; A38208; GQHRT1.
 CC DR PDB; 1TNR; 31-JUL-94.
 CC DR PDB; 1NCF; 07-DEC-95.
 CC DR PDB; 1EXT; 11-JAN-97.
 CC DR PDB; 1FT4; 12-OCT-01.
 CC DR PDB; 1ICH; 01-APR-02.
 CC DR GeneW; HGNC:11916; TNFRSF1A.
 CC DR MIM; 191190; -;
 CC DR GO; GO:0005576; C:extracellular; TAS.
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC DR GO; GO:0005032; F:tumor necrosis factor receptor, type I acti. . .; TAS.
 CC DR GO; GO:0007165; P:signal transduction; TAS.
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 CC Query Match 58.3%; Score 1517; DB 1; Length 455;
 CC Best Local Similarity 62.9%; Pred. No. 6.8e-90;
 CC Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;
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 CC DB 1 MGLSTVPDLLPLVLELVLVGIYPSGVIGLVPHLGDREKRSVCPQCKYIHPONNSTICT 60
 CC QY KCHGKTVLYNDCPPGRDTCRCVAPGTYTALENHLRCLSCSRCDPMFOVEISPCVVD 120
 CC DB 61 KCHKGTLYLNDCCPPGQDTRCEBSSGFTASBNHLRCLSCSKRKMGOVEISSCTVD 120
 CC QY 121 RDTVCGCRKNQYRYWGEYGTGRCLNCSLCPNGTVNIPQOEQDITICHGMGFPLGAKCI 180
 CC DB 121 RDTVCGCRKNQYRYWSENLECFNCSLCLNGTVHLSQGEQNTVCTCHAGFPLRENECV 180
 CC QY 181 SCHCKRK-EERKICPTRPSTGKXSOPGTTVLPVIVBELCLASPAFSAVLACRYQWK 239
 CC DB 181 SCSSCKKSLCTKCLCPDENVKGTEDSGTVLLPLVIFGLCLSLFLIGLMRYQWK 240
 CC QY 240 PKLVIICGOSTLVKEGPE-----LVVAPAGFNP-----TTICFSSPTSSSPVSIPIYI 290
 CC DB 241 SKLVIYCGKSTPEKEGELBETTTKPLAPNPSFSPPTFTGLGSPVSSITFTSSSYTT 300
 CC QY 291 SCDSNFGAVASPSSETAPPLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHL 350
 CC DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATL-----ASDPIP 335
 CC QY 351 TPVQKWEASASAPQDLADPDLVAVVGVGVPSPKWEIVRRIGLSGHEIERLENGR 410
 CC DB 336 NPLQKWEASA-HKQPSLDTDDPDLVAVENVVPLRWKEFVRRIGLSGHEIERLENGR 394

QY 411 HLEA0V5MLAMRRRTPREATLELGRVLPDMMLGCTENIERALGGAARLASEPRL 470
 DB 395 CUREA0V5MLATWRRTTREPRTXETLILGRVLPDMMLGCTEDIEBALGCPALPPAPSL 454

RESULT 4
 ID TRIA RAT STANDARD; PRT; 461 AA.
 AC P22934; Q91V30; Q91Y93;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 DE (TNF-R1) (TNF-R1) (p55)
 OS TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91090841; PubMed=1702293;
 RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
 RA Lantz M., Olsson I., Hauptmann R., Strassmann C., Adolf G.R.;
 RT "Molecular cloning and expression of human and rat tumor necrosis
 RT factor receptor chain (p60) and its soluble derivative, tumor
 RT necrosis factor-binding protein."
 RL DNA Cell Biol. 9:705-715(1990).
 [2]
 RN SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
 RP STRAIN=BB1(DR)/Mor, LEW/NHsd, ACI/Seghnd, DA/BKL, F344/NHsd, and
 RC BN/Sehnd;
 RA Furuya T., Salstrom J.L., Bina J., Hashimoto A., Dobbins D.E.,
 RA Wilder R.L., Remmers E.F.;
 RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus
 RT among autoimmune susceptible and resistant inbred rat strains."
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 CC TNFSF1/lymphotxin-alpha. The adaptor molecule FADD recruits
 CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis (by similarity).
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to
 CC homotrimerization. The aggregated death domains provide a novel
 CC molecular interface that interacts specifically with the death
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
 CC RIP and possibly FADD, are recruited to the complex by their
 CC association with TRADD. This complex activates at least two
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
 CC -1- BINDING: Binds BAg4 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.

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 CC EMBL; AF329981; AAK53567.1; -
 CC EMBL; AF329978; AAK53564.1; -
 CC EMBL; AF329979; AAK53565.1; -
 CC EMBL; AF329980; AAK53566.1; -
 CC PIR; B36555; GORP11.
 CC HSSP; P19438; INCF.
 CC InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGR_1; 3.
 DR PROSITE; PS50050; TNFR_NGR_2; 3.
 DR PROSITE; PS50017; DEATH DOMAIN; 1.
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
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 FT DOMAIN 22 211
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QY 181 SCHDC-KNKECEYLCPTPSTGKDSODPGTTVLPLVIVFGCLASFAVAVLACRQWRK 239
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QY 240 PKLYSIICQSTLVKSGPELVY-----PAGCFNT-----TTICSSTPSSS 282
 DB 241 PKLYSIICQSDAVKVEGEIVTKPLTPASIPASPNNGFNFTLGFSTTPRSHVSSST 300

QY 283 PVSIPIYISCDRNSFGAVASPSSETAPPHLKAGPILPGEPASTHLCPTGPASTHLCPTG 342
 DB 301 PIS-PVF---GPSNMENFVPVREVVPTG-GADPLLYGS-----LNVF 338

QY 343 P-PASTHLCPTPVQKWSASAPADQADPATLVAVVDGVPSPRNKELVRRIGLSEHEI 401
 DB 339 PIPA-----PVAKWEDVVAADQPORLDTADPAMLVAVVDGVPPTRWKEPMRLIGLSEHEI 392

402 ERLEIENGHRHREAOYSMLAMRRRTTREPRTLELLGVALDMDLGLCLNIEENALGAA 461
 DB 393 ERLEIENGHRHREAOYSMLAMRRRTTREPRTLELLGVALDMDLGLCLNIEENALGAA 452
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 TRIA_MOUSE STANDARD; PRT; 454 AA.
 ID TRIA_MOUSE P25118;
 AC P25118;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 DE (TNF-RI) (TNF-RI) (p55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=91187885; PubMed=1849278;
 RA Lewis M., Taragaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific."
 RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerry R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor."
 RT Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=91285014; PubMed=1647956;
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghis A.M.,
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor."
 RT Eur. J. Immunol. 21:1649-1656(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RP TISSUE=脾脏;
 RX MEDLINE=92039815; PubMed=1657766;
 RA Rother J.G., Brockhaus M., Gentz R., Lesslauer W.;
 RT "Molecular cloning and expression of the mouse Tnf receptor type b."
 RT Immunogenetics 34:338-340(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=94425292; PubMed=8188324;
 RA Bebo B.P., Linthicum D.S.;
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelial cell line."
 RT Immunogenetics 39:450-451(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=93156721; PubMed=8381516;
 RA Rother J., Bluthmann H., Gentz R., Lesslauer W., Steinmetz M.;
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene."
 RT Mol. Immunol. 30:165-175(1993).
 RN [7]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=92388257; PubMed=12477932;
 RA Krauseberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krauseberg R.L., Collins F.S., Wagner C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for TNFRSF2/TNF-alpha and homotrimeric
 CC TNFRSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
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 CC association with TRADD. This complex activates at least two
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
 CC Binds BAG4 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
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 CC EMBL; L26349; AAA39361.1; .
 CC EMBL; M76656; AAA40465.1; .
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 CC EMBL; BC004599; AAH04599.1; .
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 CC HSSP; P19438; IEXT.
 CC MGD; MGI:1314884; Tnfrsf1a.
 CC GO; GO:0007165; P:cell surface receptor linked signal transdu. .; IMP.
 CC GO; GO:0006952; P:defense response; IMP.
 CC GO; GO:0006954; P:inflammatory response; IMP.
 CC GO; GO:0007515; P:lymph gland development; IMP.
 CC InterPro; IPR000486; Death.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00531; death; 1.
 CC Pfam; PF00020; TNFR_c6; 4.
 CC SMART; SMO0005; DEATH; 1.
 CC SMART; SMO0208; TNFR; 4.
 CC PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC PROSITE; PS00650; TNFR_NGFR_2; 3.
 CC PROSITE; PS50017; DEATH_DOMAIN; 1.
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; signal.
 CC SIGNAL 1 21
 CC CHAIN 22 454
 CC DOMAIN 22 212
 CC TRANSMEM 213 235
 CC POTENTIAL.
 CC TUMOR NECROSIS FACTOR RECEPTOR
 CC SUPERFAMILY MEMBER 1A.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.

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FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 356 356 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 195 BY SIMILARITY.
FT DISULFID 185 191 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 394 394 R -> G (IN REF. 6).
SO SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 50.7%; Score 1319; DB 1; Length 454;
Best Local Similarity 56.5%; Pred. No. 2.8e-77;
Matches 268; Conservative 55; Mismatches 109; Indels 42; Gaps 12;

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DE mediating receptor TRAMP) (death domain receptor 3) (WSL protein)
DE (apoptosis inducing receptor AIR) (Apo-3) (lymphocyte associated
DE receptor of death) (LARD).
GN TNFRSF25 OR TNFRSF12 OR WSL1 OR APO3 OR DR3 OR DDR3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.
RC TISSUE=Lymphoid;
RX MEDLINE=97088617; PubMed=8934525;
RA Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
RA Githam C.J., Brown R., Farrow S.N.;
RT "A death-domain-containing receptor that mediates apoptosis.";
RL Nature 384:372-375(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Umbilical vein endothelial cells;
RX MEDLINE=97081063; PubMed=8875942;
RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
RA Duan D.R., King L., Gentz R., Ni J., Dixit V.M.;
RT "Signal transduction by DR3, a death domain-containing receptor
RT related to TNFR-1 and CD95.";
RL Science 274:990-992(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=97148200; PubMed=8994832;
RA Maresters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
RA Goddard A.D., Bauer K.D., Ashkenazi A.;
RT "Apo-3, a new member of the tumor necrosis factor receptor family,
RT contains a death domain and activates apoptosis and NF-kappa-B.";
RL Curr. Biol. 6:1669-1676(1996).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
RX MEDLINE=97227273; PubMed=9114039;
RA Screation G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
RX MEDLINE=98113360; PubMed=9446802;
RA Matzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
RA Salles G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and non-Hodgkin's lymphomas.";
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Hayashiwa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
RA Shiozawa S., Sato M., Shiozawa K., Tsukamoto Y.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 4-417 FROM N.A.
RC TISSUE=Brain, and Fetal lung;
RX MEDLINE=97205335; PubMed=9052839;
RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA Thome M., Bornand T., Hahne M., Schroeder M., Wilson A., French L.E.,
RA Browning J.L., Macdonald H.R., Teichopp J.;
RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology
RT to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL Immunity 6:79-88(1997).
RN [9]
RP SEQUENCE OF 7-417 FROM N.A.
RC TISSUE=Brain;
RA Chaudhary P.M., Hood L.E.;

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Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RN [10] INTERACTION WITH BAG4.
 RX MEDLINE=9915917; PubMed=9915703;
 RA Jiang Y., Moronicz J.D., Liu W., Goeddel D.V.;
 RT "Prevention of constitutive TNF receptor 1 signaling by silencer of
 death domain";
 RL Science 283:543-546(1999).
 CC -1- FUNCTION: Receptor for TNFRSF12/AF03L/TWEAK. Interacts directly
 with the adaptor TRADD. Mediates activation of NF-kappaB and
 induces apoptosis. May play a role in regulating lymphocyte
 homeostasis.
 CC SUBUNIT: Homodimer. Interacts strongly via the death domain with
 TRAF3 and TRADD to activate at least two distinct signaling
 cascades, apoptosis and NF-kappa-B signaling. Interacts with BAG4.
 CC SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9
 and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
 (potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=12;
 CC Name=1; Synonym=WSL-1; LARD-1A;
 CC IsoId=Q93038-1; Sequence=Displayed;
 CC Name=2; Synonym=LARD-1B;
 CC IsoId=Q93038-2; Sequence=VSP_006504;
 CC Name=3; Synonym=WSL-6L; LARD-3;
 CC IsoId=Q93038-3; Sequence=VSP_006497; VSP_006498;
 CC Name=4; Synonym=WSL-8Z; LARD-2;
 CC IsoId=Q93038-4; Sequence=VSP_006501; VSP_006502;
 CC Name=5; Synonym=LARD-4; LARD-11;
 CC IsoId=Q93038-5; Sequence=VSP_006495;
 CC Name=6; Synonym=LARD-5;
 CC IsoId=Q93038-6; Sequence=VSP_006491; VSP_006495;
 CC Name=7; Synonym=LARD-6;
 CC IsoId=Q93038-7; Sequence=VSP_006491; VSP_006493; VSP_006494;
 CC Name=8; Synonym=LARD-7;
 CC IsoId=Q93038-8; Sequence=VSP_006492;
 CC Name=9; Synonym=LARD-8;
 CC IsoId=Q93038-9; Sequence=VSP_006491;
 CC Name=10; Synonym=LARD-9;
 CC IsoId=Q93038-10; Sequence=VSP_006503;
 CC Name=11; Synonym=Beta;
 CC IsoId=Q93038-11; Sequence=VSP_006496;
 CC Name=12; Synonym=Beta soluble;
 CC IsoId=Q93038-12; Sequence=VSP_006499; VSP_006500;
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
 LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
 COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
 CC -1- PTM: GLYCOSYLATED (PROBABLY).
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -1- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine
 residue instead of arginine.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y09392; CAA70561.1; -
 DR EMBL; Y09392; CAA70559.1; -
 DR EMBL; Y09392; CAA70560.1; -
 DR EMBL; Y72763; AAC50819.1; -
 DR EMBL; U83599; AAB41434.1; -
 DR EMBL; U83600; AAB41435.1; -
 DR EMBL; U78029; AAB40918.1; -
 DR EMBL; U74611; AAB39714.1; -
 DR EMBL; U94501; AAC51306.1; -
 DR EMBL; U94504; AAC51309.1; -
 DR EMBL; U94502; AAC51307.1; -
 DR EMBL; U94503; AAC51308.1; -

DR EMBL; U94505; AAC51310.1; -
 DR EMBL; U94506; AAC51311.1; -
 DR EMBL; U94507; AAC51312.1; -
 DR EMBL; U94508; AAC51313.1; -
 DR EMBL; U94509; AAC51314.1; -
 DR EMBL; U94510; AAC51315.1; -
 DR EMBL; U94512; AAC51316.1; -
 DR EMBL; U83598; AAB41433.1; -
 DR EMBL; AF026070; AAC39556.1; -
 DR EMBL; AF026071; AAB82268.1; -
 DR EMBL; AB051850; BAB40662.1; -
 DR EMBL; AB051851; BAB40663.1; -
 DR EMBL; U75380; AAC51192.1; -
 DR EMBL; U75381; AAC51193.1; -
 DR EMBL; U83597; AAB41432.1; -
 DR EMBL; U83597; AAB41432.1; -
 DR EMBL; HGNC:11910; TNFRSF25.
 DR MIM: 603366; -
 DR GO: 0005829; C:cytosol; NAS.
 DR GO: 0005887; C:integral to plasma membrane; TAS.
 DR GO: 0016329; F:apoptosis regulator activity; NAS.
 DR GO: 0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
 DR GO: 0004872; F:receptor activity; NAS.
 DR GO: 0007166; F:cell surface receptor linked signal transdu. . . ; TAS.
 DR GO: 0006624; P:induction of apoptosis by extracellular sig. . . ; TAS.
 DR InterPro: IPR00488; Death.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00531; Death; 1.
 DR Pfam: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00050; TNFR_NGFR_2; 1.
 DR PROSITE: PS00017; DEATH_DOMAIN; 1.
 DR Receptor; Apoptosis; Transmembrane; Alternative splicing; Signal;
 KM Repeat; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 417
 FT DOMAIN 25 199 POTENTIAL.
 FT TRANSMEM 200 220 TUMOR NECROSIS FACTOR RECEPTOR
 FT REPEAT 221 417 SUPERFAMILY MEMBER 25.
 FT REPEAT 34 71 EXTRACELLULAR (POTENTIAL).
 FT REPEAT 72 115 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 116 163 TNFR-CYS 1.
 FT REPEAT 164 192 TNFR-CYS 2.
 FT REPEAT 332 413 TNFR-CYS 3.
 FT DOMAIN 332 413 TNFR-CYS 4.
 FT DISULFID 35 47 DEATH.
 FT BY SIMILARITY.

Query Match 14.9%; Score 387.5; DB 1; Length 417;
 Best Local Similarity 26.9%; Pred. No. 6,1e-18;
 Matches 130; Conservative 47; Mismatches 186; Indels 121; Gaps 18;

QY 14 VEPALLADVYPAGVQGLVHP-----GDLKREBPCKGKYNHPQNSTTCCTCKHKGYL 68
 DB 11 VAAALLVLGARGAROGGTRPCDAGDF-----HKIGLFCRCGCPAGHYL 57
 QY 69 YNDCEGRDIDCVACAGTATLENHR-RCLSCRCDEMPQVETSPCVDDDTGVC 127
 DB 58 KAPCTPCGNSCTLYCPQDTFLAMENHNSECARQADDEASQALNCAVADTRGCG 117
 QY 128 RKN-----QYREYGEETGFRCLNSLCPNGTVN-----IPCEODDTIC-HGMEGFLNGA 177
 DB 118 KPGMFVECOVSGCVSSSPFYCQPLDC--GALHNHRLLC--SRDIDCGTCLPGEYENG 174
 QY 176 KCTSC-----HDCKKCEKLCPTRPSTGKSDQDPGTTVLLPLVYFGLCLASPAVVLA 232
 DB 175 GCVSCPTSLGSCPER-CAAVCGWR-----QMFVVQVLLAGLVVPLLGATLT 221
 QY 233 CRVOR-WKPKLYSIICGSLTVKGEPELVAPAGFNPNTTICSSSPSSSPVSIPIYIS 291
 DB 222 YTHRCNPKR-----PLVT 235
 QY 292 CDRNFGAVASPSETAPPHLKAGRIIPGPASTHLCTPGPASTHLCTPGPASTHLCT 351
 DB 236 ADEAGMEALTPRPATHTSLPDSATLLAPDSSSKICTGVGVGNS--WTPGVPTGQALC 293

QY 352 EVOKM-----EASAPADPOLADADA-----TIYAVDGVPPSRKELVER 393
DB 294 FOVTWMDQLPSRALGPAAPTLSPSPAGSPAMMLQOPOLYDMDAVPARMRKEFYRT 353
OY 394 IGLSPHEIRLELNGRHLEAOVSMILAMRRTRRATTELGRVLRDMLGCLLENI 453
DB 354 IGLHEAELEAVEVEIGR-FRDOYEMLRKROQP--AGIGAVYAAALERMGLDGCVEDL 409
QY 454 BEAL 457
DB 410 RSRL 413
RESULT 7
ID 110B HUMAN STANDARD; PRT: 440 AA.
AC 014763; 014720; 015508; 015517; 015531; 09BVE0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 2) (TRAIL-R2)
DE receptor-2) (TRAIL-R2)
CN TRNRS10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF N-TERMINUS.
RC TISSUE=Forebrain Fibroblast;
RX MEDLINE=97455925; PubMed=9311998;
RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y., Bolani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A., Goodwin R.G., Rauch C.T.;
RA "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";
RT EMO J. 16:5386-5397(1997).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND ALTERNATIVE SPLICING.
RC TISSUE=Liver;
RX MEDLINE=97431692; PubMed=9285725;
RA McMichael A., Bell J.I.;
RT "TRICK2, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL.";
RL Curr. Biol. 7:693-696(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND CHARACTERIZATION.
RC TISSUE=Liver, and Spleen;
RX MEDLINE=9603016; PubMed=9373179;
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N., Tschopp J.;
RT "Characterization of two receptors for TRAIL.";
RL FEBS Lett. 416:329-334(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Ovary;
RX MEDLINE=97467719; PubMed=9326928;
RA Wu G.S., Burns T.F., McDonald E.R. II, Jiang W., Meng R., Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R., Spilner N.B., Markowitz S., Wu G., el-Deiry W.S.;
RT "Killer/DR5 is a DNA damage-inducible p53-regulated death receptor gene.";
RL Nat. Genet. 17:141-143(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=97390508; PubMed=9242610;
RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;
RT "An antagonist decoy receptor and a death domain-containing receptor for TRAIL.";
RL Science 277:815-818(1997).
RN [6]

RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=97467318; PubMed=9325248;
RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;
RT "Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL.";
RL J. Biol. Chem. 272:25417-25420(1997).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=96090092; PubMed=9430227;
RA Chaudhary P.M., Eby M., Jassim A., Bookwalter A., Murray J., Hood L.;
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway.";
RL Immunity 7:821-830(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=97390509; PubMed=9242611;
RA Sheridan J.P., Masters S.A., Picti R.M., Gurney A., Skubatch M., Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I., Goddard A.D., Godowski P., Ashkenazi A.;
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy receptors.";
RL Science 277:818-821(1997).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yusa Y.;
RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2 gene in colorectal carcinoma.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RA Cao X., Zhang W., Wan T.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RA Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;
RT "Homo sapiens homolog of tumor necrosis factor receptor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Cervix;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins L., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stempleton W., Soares W.B., Bonaldo M.F., Casavant T.V., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E., Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.
RX MEDLINE=20017054; PubMed=10549288;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5.";
RL Mol. Cell 4:563-571(1999).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.
RX PubMed=10542098;

RA Mongkolkeha J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Sreeton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RT specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFSP10/TRAIL. The
 CC adaptor molecule FADD recruits caspase-8 to the activated
 CC receptor. The resulting death-inducing signaling complex (DISC)
 CC performs caspase-8 proteolytic activation which initiates the
 CC subsequent cascade of caspases (separate-specific cysteine
 CC proteases) mediating apoptosis. Promotes the activation of NF-
 CC kappaB.
 CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Long; Synonym=TRICK2B;
 CC IsoId=O14763-1; Sequence=Displayed;
 CC Name=Short; Synonym=TRICK2A;
 CC IsoId=O14763-2; Sequence=VSP_006490;
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;
 CC very highly expressed in tumor cell lines such as HeLa S3, K562,
 CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral
 CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,
 CC ovary, uterus, placenta, testis, esophagus, stomach and throughout
 CC the intestinal tract; not detectable in brain.
 CC -1- INDUCTION: TNFSP10B is regulated by the tumor suppressor p53.
 CC -1- DISEASE: Defects in TNFSP10B may be a cause of squamous cell
 CC carcinoma of the head and neck.
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -----
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 CC -----
 DR EMBL AF016849; AAC51778.1; -
 DR EMBL AF018657; AAB70577.1; -
 DR EMBL AF018658; AAB70578.1; -
 DR EMBL AF016266; AAB81180.1; -
 DR EMBL AF022386; AAB71949.1; -
 DR EMBL AF022628; AAB67109.1; -
 DR EMBL AF020501; AAB71412.1; -
 DR EMBL AF016268; AAC01565.1; -
 DR EMBL AF012535; AAB67103.1; -
 DR EMBL AB014718; BAA33723.1; -
 DR EMBL AB014710; BAA33723.1; JOINED.
 DR EMBL AB014712; BAA33723.1; JOINED.
 DR EMBL AB014712; BAA33723.1; JOINED.
 DR EMBL AB014713; BAA33723.1; JOINED.
 DR EMBL AB014714; BAA33723.1; JOINED.
 DR EMBL AB014715; BAA33723.1; JOINED.
 DR EMBL AB014716; BAA33723.1; JOINED.
 DR EMBL AB014717; BAA33723.1; JOINED.
 DR EMBL AF153687; AAF75587.1; -
 DR EMBL AF192548; AAF07175.1; -
 DR EMBL BC001281; AAH01281.1; -
 DR PDB: 1D0G; 22-OCT-99.
 DR PDB: 1D4V; 01-NOV-99.
 DR GeneW; HGNC:11905; TNFRSF10B.
 DR MIM; 603612; -
 DR GO: GO:0016021; C: integral to membrane; IC.
 DR GO: GO:0016506; F: apoptosis activator activity; NAS.
 DR GO: GO:0008655; F: caspase activator activity; NAS.
 DR GO: GO:0004872; F: receptor activity; NAS.
 Query Match 10.4%; Score 271.5; DB 1; Length 440;
 Best Local Similarity 25.5%; Pred. No. 1.6e-10;

Matches 123; Conservative 57; Mismatches 196; Indels 107; Gaps 25;
 QY 4 PTVPGLLLPLVPLADVPRAGVGVPHRQDLEKRSPPCKGKYNHPOKSTICTCH 63
 DB 32 PRVPTLLVVAAYLL---VSAESAITOODLAPQGRAPQQRSSPSGL-----CP 82
 QY 64 KGTLYNDPCPGRDTRCVPAPG-TYALENHRLCLSCRCRDEMVEISPCVDND 122
 DB 83 PGHHISD---GR-DCISRYGQDYS THNNDLFLCRLCRC--DSEVELSPCTTRN 134
 QY 123 TVCCGRKNQYREYWGERTFRCLNSL-CPNGTVNI-PCQERODTIC-HCHMGFLKAKC 179
 DB 135 TVCCCEBGTFRF--EDSEPMCKRCRTGCPRMGVYGDCTTPMSDIECYKESG----- 184
 QY 180 ISCHDCKKKECEKLCPRPSRSGKXSODPGTVLPLVLPGLCLASFAV--VLACRYQR 237
 DB 185 -TKISGEPAVEEVTSSPGT-----PASCSLSGIII-DVTAAYVLIYAVFYCKSL 236
 QY 238 WK---PKLYSIICGSTLVKEGEPELVAPAGFNPPTTICFSPSSPSVSIPIYISCDR 294
 DB 237 WKYVLPYIKGICSGSG-----GDPERV-----DR 260
 QY 295 SNFGAVASPSSETAPPHLKAPILPG--PPASTHLCPPGPPASTHLCPPGPPASTHLC 352
 DB 261 SS---QRPAGBDVNLNIVSIILOPTQVPEQEMEVEQEPAPPTGVNMLSPG--ESEHLLP 314
 QY 353 VQKKEASAPSPDOLADNPA-TLYAVDGS---VPERKVELVRLGLSHEIERLE 407
 DB 315 AEARSQRRLLVPAWEDPTETURQCFDPAFLVPEDSWPMLKKGLMNEIVAAAE 374
 QY 408 NGRHLREAOYVSNLAAMRRTPRRATLELLGRVLRDMDLCLLENIBALGAARLASBP 467
 DB 375 AAGH-RDILYMLIKMVKKT-----GRDASVHTLLALBETLSGRL---AKOKIED 420
 QY 468 RLL 470
 DB 421 HLL 423
 RESULT 8
 TRN3_HUMAN STANDARD; PRT; 435 AA.
 AC P36941;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
 DE protein) (Tumor necrosis factor C receptor).
 DE LTR OR TNFRSF3 OR TNFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93252381; PubMed=8486360;
 RA Baens M., Chaffanet M., Casilman J.J., den Berghe H., Marynen P.;
 RT "Construction and evaluation of a hncDNA library of human l2p
 RT transcribed sequences derived from a somatic cell hybrid.";
 RL Genomics 16:214-218(1993).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen G.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Datschenko L., Marubini K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [3]
 RP FUNCTION.
 RX MEDLINE=94225209; PubMed=8171323;
 RA Crowe P.D., Vamvakis T.L., Walter B.N., Ware C.F., Heselin C.,
 RA Ehrenfele B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.,
 RT "A lymphotoxin-beta-specific receptor.",
 RL Science 264:707-710(1994).
 [4]
 RP CHARACTERIZATION.
 RX MEDLINE=9923511; PubMed=10207006;
 RA Mu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.,
 RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 RT death in HeLa cells.",
 RL J. Biol. Chem. 274:11868-11873(1999).
 [5]
 RP FUNCTION.
 RX MEDLINE=20261554; PubMed=10799510;
 RA Rooney I.A., Butrovich K.D., Glaes A.A., Borboghlu S., Benedict C.A.,
 RA Wolbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.,
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 RT LIGHT-mediated apoptosis of tumor cells.",
 RL J. Biol. Chem. 275:14307-14315(2000).
 [6]
 RP INTERACTION WITH TRAF3.
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbot L., Ware C.F.,
 RA Yagita H., Okumura K.,
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
 RT the lymphotoxin-beta receptor.",
 RL J. Biol. Chem. 271:14661-14664(1996).
 [7]
 RP INTERACTION WITH TRAF4.
 RX PubMed=9626059;
 RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
 RA Gascogne R.D., Berern K., McFadden D., Shabalik A., Hugh J.,
 RA Reynolds A., Cleveland C.V., Reed J.C.,
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
 RT adult, fetal, and tumor tissues.",
 RL Am. J. Pathol. 152:1549-1561(1996).
 [8]
 RP INTERACTION WITH TRAF5.
 RX MEDLINE=98172745; PubMed=9511754;
 RA Mizushima S.-I., Fujita M., Ichida T., Azuma S., Kato K., Hirai M.,
 RA Otsuka M., Yamamoto T., Inoue J.-I.,
 RT "Cloning and characterization of a cDNA encoding the human homolog of
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).",
 RL Gene 207:135-140(1998).
 [9]
 RP FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs.
 CC -1- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR EMBL: L04270; AAA36757.1; -
 DR EMBL: BC026262; AAH26262.1; -
 DR PIR: I54182; I54182.
 DR HSSP: P25942; ICDP.
 DR Genew: HGNC:6718; LTR.
 DR MIM: 600979; -
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR001368; TNFR_C6.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 435
 FT
 FT DOMAIN 31 227
 FT TRANSMEM 228 248
 FT DOMAIN 249 435
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 168
 FT REPEAT 169 211
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 148
 FT DISULFID 142 167
 FT DISULFID 170 185
 FT CARBOHYD 40 40
 FT CARBOHYD 177 177
 SQ SEQUENCE 435 AA; 46709 MM; 624626E6022P656F CRC64;
 Query Match 9.9%; Score 257; DB 1; Length 435;
 Best local similarity 27.3%; Pred. No. 1.3e-09;
 Matches 121; Conservative 37; Mismatches 158; Indels 128; Gaps 25;
 1 MGLP---TVPGILV-PLVP--ALLADVPAGVGLVHPGDEKRESPPCGKYNHPOH 54
 1 MLFPAISARGLAGPLVILGFLAASQPAV-----PLASNQCRDQEKRYEYEPH 55
 55 STICTCKCHKGTLYLNDPCGGRDTRVCAPGTYTALBNHLRCLSCRCRDEMPOVEI 114
 56 -RICSCRCPGTYVSAC-SRIRDTVCATCENSYNHMMVLTICQCRPCDPVWGLEI 113
 115 SPQVVDYVCGCKKQYREYWGEGRCVCLNSL---CPKCTVVIPOERODIT----- 165
 114 APTSKRRTQCRCPGMFCAM--ALECTHCCLSDCPETE-----AELDEVGKNNH 166
 166 -CHCHMGFPFLK---GAKTISCCHDCKKCEKCLCP---TRPSGKDSQDP-----GT-- 209
 167 CVPKKAHPONTSSPSARCQPHRCENQGLVEAHPGASQDTTKNPLRPPMSGTM 226
 210 --TVLPLVIVFGCLASFASVVLACRYORKPKLYSIIQGSQTLVKEGEBELVPAFG 267
 227 MLAVLPLP--AFPLLATVFSCL-----WKS--HPSLCKKGLSKLRPQ-----GEGP 271
 268 NPTTITFPSSRPSSPSISIPY-----ISCDS--NFGAVAPSSSTAP----- 310
 272 NPV-----AGSWEPKAPHYFPDLVQPLLPISGDVSPVSTGLPAAPVLEAGVPOOSP 324
 311 -----HLKAGPLPAPPASTHL-CTPGP 332
 325 LDLTREQLBREGSOVAHNGTNGHVTGSGMTTNGNIVTNGVPLGSPPGSGDLPATPEP 384
 333 P-ASTHLCTPGPPASTHLCTPVOK 355

DB 385 PVP1PEEGDPPGPPG--LSTPHOE 405

RESULT 9

TNR3 MOUSE STANDARD; PRT; 415 AA.

AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 GN LTRB OR TNFRSF3 OR TNFCR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Browning J.L., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 and expression."
 RL J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 sequence trap and chromosomal mapping."
 RL Genomics 30:312-319(1995).
 RN [3]
 RP INTERACTION WITH TRAF5.
 RC STRAIN=BALB/c;
 RX MEDLINE=96276943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
 the lymphotoxin-beta receptor."
 RL J. Biol. Chem. 271:14661-14664(1996).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 LTR and LTRB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 and TRAF5. May play a role in the development of lymphoid organs
 (By similarity).
 CC -1- SUBUNIT: Self-associates (By similarity). Associates with TRAF3.
 CC Associates with TRAF3 and TRAF4 (By similarity).
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; U29173; AAA68964.1; .
 DR EMBL; L38423; AA00846.1; .
 DR EMBL; U30798; AAA81334.1; .
 DR HSSP; O14763; 100G.
 DR MCD; MG1104875; LdbR.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR SMART; SMO0208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00652; TNFR_NGFR_2; 3.
 KM Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415 TUMOR NECROSIS FACTOR RECEPTOR

FT DOMAIN 31 223 SUPERFAMILY MEMBER 3.
 FT TRANSMEM 224 244 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 81 TNFR-CYS 1.
 FT REPEAT 82 124 TNFR-CYS 2.
 FT REPEAT 125 170 TNFR-CYS 3.
 FT REPEAT 171 213 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 142 169 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 415 AA; 44956 MM; 298326A56AEF661 CRC64;

Query Match 9.5%; Score 247; DB 1; Length 415;
 Best Local Similarity 25.8%; Pred. No. 5.5e-09;
 Matches 105; Conservative 46; Mismatches 168; Indels 88; Gaps 20;

QY 12 PLVPLALLADVPYAGVGLVPHPDLEKRESPCQCKKNHPQNTICTCKHGTLYND 71
 DB 16 PLLLG--LSGLVLSQPLVP--PRIENQTCWDQKEYEPMHD--VCCSRCPGEFVAV 71
 QY 72 CPFGPDTCVCVAGTYTALENLRCLSCSRDEMFQVEISPCVVDRTVCGCRNQ 131
 DB 72 C-SNSQDTVCCTCHNSGNEHNMNLSTCOLCRPDIVLGFPEVAPCTSDRAEBCRCQGM 130
 QY 132 YREYWGTEGFRCLNS---LCPNGTNIPQGERDITCH--CHMGFPLK---GAKC 179
 DB 131 SCVLLDN---ECVACEERVLVCPGTEAEVTDEIMDVNVCVCKRGHPQNTSSPRAC 187
 QY 180 ISCHDCKNKEBKLCPTRPSTG-----KSDQDGTVLLPLVVFGLCLASPAVYLAC 233
 DB 188 QPHTRC---ETQGLVEAAPGYSYDTICKNPEFGAML--LAILSLVFLFTTVLAC 242
 QY 234 RYQWRKPKLYSIICGO-STLVK---EGEPDLVPAQFNP-----TTTICFSSTPSSSP 283
 DB 243 AMWR-----HSLRKIKGTLKRPGESESPCAPAPADPHFPLABEILPMSDLSFSP 297
 QY 284 VSIPT-----YISCDRNSFGAVASPS-----SETAPPHIKA 314
 DB 298 AGPTAPSLERVLQOOSPLVOARELEAPGEHGVHGANGINVTGQSVTVTGNIYVN 357
 QY 315 GPLPFG-----PPASTHLCTGPPASTHLCTPPASTHLCTPVOK 355
 DB 358 GPVLGTRGPGDPPA-----PPEPPYPTP--EBGAPGSELSTVYOE 397

RESULT 10
 TR16 HUMAN STANDARD; PRT; 427 AA.
 ID TR16_HUMAN
 AC P08138;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-SEP-2003 (Rel. 08, Last sequence update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
 affinity nerve growth factor receptor) (NGF receptor) (gp80-LNFR)
 GN NGFR OR TNFRSF16.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87051725; PubMed=3022937;

RA Johnson D., Lanahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
 RA Botwell M., Chao M.;
 RT "Expression and structure of the human NGF receptor.";
 RL Cell 47:545-554(1986).
 RN (2)
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=6906903; PubMed=2850481;
 RA Sehgal A., Patil N., Chao M.;
 RT "A constitutive promoter directs expression of the nerve growth factor
 RT receptor gene.";
 RL Mol. Cell. Biol. 8:3160-3167(1988).
 RN (3)
 RP INTERACTION WITH TRAF2, TRAF4 AND TRAF6.
 RX PubMed=10514511;
 RA Ye X., Mehlén P., Rabizadeh S., VanArsdale T., Zhang H., Shin H.,
 RA Wang J.J., Leo E., Zapata J.M., Hauser C.A., Reed J.C., Bredesen D.E.;
 RT "TRAF family proteins interact with the common neurotrophin receptor
 RT and modulate apoptosis induction.";
 RL J. Biol. Chem. 274:30202-30208(1999).
 RN (4)
 RP INTERACTION WITH TRAF6.
 RX PubMed=9915784;
 RA Khursigara G., Orlinick J.R., Chao M.V.;
 RT "Association of the p75 neurotrophin receptor with TRAF6.";
 RL J. Biol. Chem. 274:2597-2600(1999).
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
 CC and NT-4. Can mediate cell survival as well as cell death of
 CC neural cells.
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 CC associated cell death executor. Interacts with TRAF2, TRAF4 and
 CC TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: N- AND O-glycosylated.
 CC -1- PTM: Phosphorylated on serine residues.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
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FT REPEAT 148 188 TNFR-CYS 4.
 FT DOMAIN 344 421 DEATH.
 FT DOMAIN 197 248 SER/THR-RICH.
 FT DISULFID 32 43 BY SIMILARITY.
 FT DISULFID 44 57 BY SIMILARITY.
 FT DISULFID 47 64 BY SIMILARITY.
 FT DISULFID 67 83 BY SIMILARITY.
 FT DISULFID 86 99 BY SIMILARITY.
 FT DISULFID 89 107 BY SIMILARITY.
 FT DISULFID 109 122 BY SIMILARITY.
 FT DISULFID 125 138 BY SIMILARITY.
 FT DISULFID 128 146 BY SIMILARITY.
 FT DISULFID 149 164 BY SIMILARITY.
 FT DISULFID 167 180 BY SIMILARITY.
 FT DISULFID 170 188 BY SIMILARITY.
 FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).
 SO SEQUENCE 427 AA; 45183 MW; 809FAL43FB3D625B CRC64;
 Query Match 9.1%; Score 236; DB 1; Length 427;
 Best Local Similarity 22.9%; Pred. No. 2.8e-08;
 Matches 111; Conservative 62; Mismatches 194; Indels 118; Gaps 22;
 QY 7 PGLLPVLPVLPALADVPAGVQGLVPHPGDLKRESPCPGKXNHPNMTICCTCKHGT 66
 DB 13 PRLILLILGVSLGKAEK-----CPGLVYTH--SGECKACNLGE 51
 QY 67 YLVNDGCGPDRDTCRCVARG-TYTALENLRCLSCSRCDMPQVEISPCVVDPTVC 125
 DB 52 GVAQPC--GANQTVCEPCLDSVTFSDVSAITEPKCTECVG--IQSMGAPVEADAVC 107
 QY 126 GCRKNQRYEYGEYGFRCNLSLCPNGT-VNIPQERODTIC-HCHMGFFLKAK-----C 179
 DB 108 RC---ANGYQDETTGRCACRCVCSGSLVFCQKQNTVEECDDGYSDAANVDC 164
 QY 180 ISCHDK-----NKECEKLCPT-----PSTGSDQDPCTVLLPLVIVRG 220
 DB 165 LPTVCEDETEROLRECTRWADACEBI-PGRWITRSTPEGSDTAPSTOE--PEAPPEQ 221
 QY 221 LCLASFVVLACRYQRMWPKYSLICQSTLYKEBEPELVAPGFNPTTTCFSTGS 280
 DB 222 DLASTVAVGVY-----TWGSSOPVTRGTNNLPLV-----YCSILA 260
 QY 281 SSPVSIPPYI-----SCDRSNGAVASPSSETAPP-----HLKAGPILGPPASTHLC 329
 DB 261 AAVVGLVAVYIAFRKMSCKQKQGANRPVQTPPEBGEKLHSDG--ISVDSGLHDOQ 318
 QY 330 PGPASTHLCPTPPASTHLCPTPVQKREASAPSDQLADADPATLYAVVDGVPSPRWE 389
 DB 319 PHTQTASGQALKKGGLVSLPAPKREVE-----KILNSAGDPTMR 361
 QY 390 LVARLLGLS-EHEIERLENGHRLREAOYSMLAAMRRTPREARETEHLGRVLKMDLLG 448
 DB 362 LAGELLYQPEH-----IDFTHEACPVRLALSW--ATQSATLLALLAALRLRIORD 412
 QY 449 CLENT 453
 DB 413 LVESL 417
 RESULT 11
 TR16_RAT
 ID TR16_RAT STANDARD; PRT; 425 AA.
 AC P07174;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
 GN NGFR OR TNFRSF16.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

CC NCBI_Taxid=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8711589; PubMed=3027580;
 RA Radeke M.J., Misko T.P., Han C., Herzenberg L.A., Shooter E.M.;
 RT "Gene transfer and molecular cloning of the rat nerve growth factor
 receptor.";
 RL Nature 325:593-597 (1987).
 RN (2)
 RP SEQUENCE OF 1-22 FROM N.A.
 RX TISSUEALIVER;
 RA MEDLINE=9307038; PubMed=1446821;
 RA Metcalf W., Tammak T., Allikmets R., Saarma M., Pearson H.;
 RT "Regulatory elements and transcriptional regulation by testosterone
 and retinoic acid of the rat nerve growth factor receptor promoter.";
 RL Gene 121:247-254 (1992).
 RN (3)
 RP STRUCTURE BY NMR OF 334-418.
 RX MEDLINE=97449145; PubMed=9305641;
 RA Liepinsh E., Ilag L.V., Oetting G., Ibanez C.F.;
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
 RL EMBO J. 16:4999-5005 (1997).
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
 and NT-4. Can mediate cell survival as well as cell death of
 neural cells.
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 associated cell death executor. Interacts with TRAF2, TRAF4 and
 TRAF6 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: N- AND O-glycosylated.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
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 CC -----
 DR EMBL: X05137; CAA28783.1.
 DR EMBL: X61259; NOT_ANNOTATED_CDS.
 DR PIR: A26431; A26431.
 DR PDB: INGR; 29-JUL-97.
 DR InterPro: IPR000468; Death.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PR00531; death_1.
 DR Pfam: PR00020; TNFR_C6; 4.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00650; TNFR_NGFR_2; 4.
 DR PROSITE: PS50017; DEATH DOMAIN; 1.
 KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
 KW Repeat; Phosphorylation; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 425
 FT DOMAIN 30 251
 FT TRANSMEM 252 273
 FT DOMAIN 274 425
 FT REPEAT 32 65
 FT REPEAT 67 108
 FT REPEAT 109 147
 FT REPEAT 149 189
 FT DOMAIN 354 419
 FT DOMAIN 198 249
 FT DISULFID 33 44
 FT DISULFID 45 58
 FT DISULFID 48 65
 FT DISULFID 68 84

FT DISULFID 87 100 BY SIMILARITY.
 FT DISULFID 90 108 BY SIMILARITY.
 FT DISULFID 110 123 BY SIMILARITY.
 FT DISULFID 126 139 BY SIMILARITY.
 FT DISULFID 129 147 BY SIMILARITY.
 FT DISULFID 150 165 BY SIMILARITY.
 FT DISULFID 168 181 BY SIMILARITY.
 FT DISULFID 171 189 BY SIMILARITY.
 FT CARBOHYD 61 61
 FT CARBOHYD 71 71
 SQ SEQUENCE 425 AA; 45432 MW; B2E152094D3827F8 CRC64;
 Query Match 8.74; Score 227.5; DB 1; Length 425;
 Best Local Similarity 23.44; Pred. No. 9.8e-08;
 Matches 107; Conservative 59; Mismatches 169; Indels 123; Gaps 24;
 44 CPOGKYNHPQNSTICTCKHKGYLYNDGPGPRDIDCRVCAFG-TYTALENHLRLCLSC 102
 33 CSTGLYTH---SGECRCACNIGEVAPQC--GANQVCEPCLDNVTFSDVASATEPCPC 87
 103 SRCDENFQVEISPCVDRTVCGCRNQYREYWGTFPRCLNCSLCPNGT-VNIPQGR 161
 88 TECUG--LQSMASACVADDAVCRGAYGYOD--ETG-HCEACSVCEVSGLVPSQDK 142
 162 QDTIC-HCHMGPFKAKGAK---CISCHCKKCEKCLPTPSTGKSDQ-PGTVLLPL 215
 143 QNTVCECPGEGTYSDEANHYDPCLPCTVCEDE-RLQRECTPMADACEEIPG----- 194
 216 VIVFGCLIASFASVLAACRYQWKPKLYSIICGOSTLVKEGEBL---LVPAFGNPT 270
 195 -----RWIPRSTPPEGSSTAPSTQBEVPEEDLVSTVADMV 233
 271 TTICFSSTP-----SSSPVSIPIYI-----SCDRSNPGVAASPSSE 306
 234 TTWVGSSQPVVTRGTNDLIPVYSIIAAVVGIVAVIARKNRNSCKQNGANSRPVNO 293
 307 TAPP-----HLKAPILPGPASTHLCTPGPASTHLCTPPA-----STHLCTPVQWK 356
 294 TPPEGKRLSDSG--ISVDSGLH-----DQTHQTNSGQLKDGNYLSLPLTKR 345
 357 EASAPSAADQADADPATLVAVVDGVPSPKKEIVRLGIS-EIEIRLBLENRHLREA 415
 346 E-----EVEKLLND-----TWRIHAGELGYQPEH-----IDSFTHACP 380
 416 QYSMLAARRRTPRREATLELGRVLRDMDLGLCTENI 453
 381 VRLALSWGAD---SATDLALALAKRIQADIVESL 415
 RESULT 12
 TR16_MOUSE STANDARD: PRT: 417 AA.
 ID TR16_MOUSE
 AC 0920W1.
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
 DE affinity nerve growth factor receptor) (NGF receptor) (low affinity
 DE neurotrophin receptor p75NTR).
 GN NGFR OR TNFRSF16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=A;
 RX MEDLINE=99077793; PubMed=9857182;
 RA Tuffreau C., Benejean J., Blondel D., Kieffer B., Flamand A.;
 RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
 RT receptor for rabies virus.";
 RL EMBO J. 17:7250-7259 (1998).
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,

CC AND NT-4. Can mediate cell survival as well as cell death of
 CC neural cells (By similarity). Binds to rabies virus glycoprotein
 CC Gs.
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 CC associated cell death executor. Interacts with TRAF2, TRAF4 and
 CC TRAF6 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- PTM: N- AND O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylated on serine residues (By similarity).
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sdb.cn/announce/>
 CC or send an email to license@isb-sdb.cn).
 CC -----
 CC EMBL: AF105292; AAD17943.1; -
 CC HSSP: P07174; INGR.
 CC DR MGD; MGI:97323; Ngfr.
 CC DR GO; GO:0005035; F:death receptor activity; IDA
 CC DR GO; GO:0005515; F:protein binding activity; IPI.
 CC DR GO; GO:0007411; P:axon guidance; IMP.
 CC DR GO; GO:0007417; P:central nervous system development; IMP.
 CC DR GO; GO:0006917; P:induction of apoptosis; IDA.
 CC DR InterPro: IPR004488; Death.
 CC DR InterPro: IPR013368; TNFR_C6.
 CC DR Pfam: PF00531; death_1.
 CC DR Pfam: PF00020; TNFR_C6; 4.
 CC DR SMART; SM00005; DEATH; 1.
 CC DR SMART; SM00208; TNFR; 3.
 CC DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC DR PROSITE; PS00650; TNFR_NGFR_2; 4.
 CC DR PROSITE; PS0017; DEATH DOMAIN; 1.
 CC KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
 CC Repeat; Signal.
 CC FT CHAIN 1 21 BY SIMILARITY.
 CC FT 22 417 TUMOR NECROSIS FACTOR RECEPTOR
 CC FT DOMAIN 22 246 SUPERFAMILY MEMBER 16.
 CC FT TRANSMEM 247 265 EXTRACELLULAR (POTENTIAL).
 CC FT 266 417 POTENTIAL.
 CC FT REPEAT 24 57 CYTOPLASMIC (POTENTIAL).
 CC FT REPEAT 51 100 TNFR-CYS 1.
 CC FT REPEAT 101 139 TNFR-CYS 2.
 CC FT REPEAT 141 181 TNFR-CYS 3.
 CC FT REPEAT 141 181 TNFR-CYS 4.
 CC FT DOMAIN 346 411 DEATH.
 CC FT 190 241 SER/THR-RICH.
 CC FT DISULFID 25 36 BY SIMILARITY.
 CC FT DISULFID 37 50 BY SIMILARITY.
 CC FT DISULFID 40 57 BY SIMILARITY.
 CC FT DISULFID 60 76 BY SIMILARITY.
 CC FT DISULFID 79 92 BY SIMILARITY.
 CC FT DISULFID 82 100 BY SIMILARITY.
 CC FT DISULFID 102 115 BY SIMILARITY.
 CC FT DISULFID 118 131 BY SIMILARITY.
 CC FT DISULFID 121 139 BY SIMILARITY.
 CC FT DISULFID 142 157 BY SIMILARITY.
 CC FT DISULFID 160 173 BY SIMILARITY.
 CC FT DISULFID 163 181 BY SIMILARITY.
 CC FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 417 AA; 44686 MW; 5D7A510DBA9B2 CRC64;
 CC -----
 CC Query Match 8.5%; Score 221.5; DB 1; Length 417;
 CC Best Local Similarity 23.1%; Pred. No. 2.3e-07;
 CC Matches 106; Conservative 63; Mismatches 166; Indels 123; Gaps 26;
 CC 44 CPOKYNHPSNSTICCKKCHKGYLVNDGCGPGEDDCRCVCAFG-TYTALENHARCLSC 102
 CC 25 CSTGMYTH---SGECCKACNIGEGVAPC--GANOTVCEPCLDLSVFSDVSVATEPCCKPC 79

OY 103 SRCDENPQVSIKCYVDROVCCGRKQRYREYGEFRCLNSLCPNGT-VNIPQOER 161
 DB 80 TECGQ-LQSNASACVENDAVCRCSGYVOD--EEYG-RCEACSVGSGSLVFSQDK 134
 OY 162 QDTIC-HCHMGFFPKGAK---CISCHCK-----NKEGKLCPR----- 197
 DB 135 QNTVCERCBEPTYDEANRNDPLCTVCEDETERQLRECTPMADABCEET-PCGWITRST 193
 OY 198 PSTKRD-----SQDGTTVLLPLVIVFGLCLASFVAVLACRYQWRMKYSLICQOSTL 252
 DB 194 PPEGSDVTTSTQRPAPPRDLI-----ASTV-----ADVTYTMGSSQPV 225
 OY 253 VKGEPEPLVAPAFNFTTTCBSSTSSSPVSIPIY-----SCDRNFGAVASPSSE 306
 DB 236 VTRGTADNLLPV-----YCSIIAAVGVGVAVIAFRKWNKCKOKGANSRPVQ 285
 OY 307 TAPP-----HUKAGPILPGPASTHLCPTGPASTHLCPTGPAP-----STHLCPTQKW 356
 DB 286 TPPEGEKHSDSG--ISVDSGLH-----DQHTQTASAQALKGDKNLYSLPLTKR 337
 OY 357 EASAPSPDQADADPATYAVVDGVPSPRWKELVERLAGS-EHEYERLENGRHLEA 415
 DB 338 E-----EVEKLLNGD-----TWRIHAGELGQVPEH-----IDSFTEACP 372
 OY 416 QYSMLAARRRRTPREATTLELGRVLRDMDLACLENI 453
 DB 373 VRALLMSWGAOD---SATLDALLAALRRIORADIVESL 407
 RESULT 13
 ID TR16 CHICK STANDARD; PRT; 416 AA.
 AC P16519;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
 DE (975 ICD) (low affinity neurotrophin receptor p75NTR).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90166579; PubMed=2560385;
 RA Large T.H., Weiskamp G., Heider J.C., Radeke M.J., Misko T.P.,
 RA Shooter E.M., Reichardt L.F.;
 RT "Structure and developmental expression of the nerve growth factor
 RT receptor in the chicken central nervous system.";
 RL Neuron 2:1123-1134(1989).
 RN [2]
 RP SEQUENCE OF 21-416 FROM N.A.
 RX MEDLINE=90152140; PubMed=2154393;
 RA Heuer J.G., Pateme-Nainte S., Wheeler E.F., Botwell M.;
 RT "Structure and developmental expression of the chicken NGF receptor.";
 RL Dev. Biol. 137:287-304(1990).
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
 CC and NT-4. Can mediate cell survival as well as cell death of
 CC neural cells (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 CC associated cell death executor. Interacts with TRAF2, TRAF4 and
 CC TRAF6 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: N- AND O-glycosylated.
 CC -1- PTM: Phosphorylated on serine residues.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
 DR PIR; JN0006; JN0006.

DR HSBD, P07174; INGR.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR01368; TNFR_c6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
 KW Repeat; Phosphorylation; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 416
 FT
 FT DOMAIN 29 239
 FT TRANSMEM 240 261
 FT DOMAIN 262 416
 FT REPEAT 23 57
 FT REPEAT 58 99
 FT REPEAT 100 138
 FT REPEAT 140 180
 FT DOMAIN 333 410
 FT TRANSMEM 188 236
 FT DOMAIN 24 35
 FT DISULFID 36 49
 FT DISULFID 39 56
 FT DISULFID 59 75
 FT DISULFID 78 91
 FT DISULFID 81 99
 FT DISULFID 101 114
 FT DISULFID 117 130
 FT DISULFID 120 138
 FT DISULFID 141 156
 FT DISULFID 159 172
 FT DISULFID 162 180
 FT CARBOHYD 52 52
 FT CONFLICT 36 36
 FT CONFLICT 173 173
 FT CONFLICT 276 276
 FT CONFLICT 396 396
 FT SEQUENCE 416 AA; 44654 MW; 6BCBAA54FAD2D056 CRC64;
 Query Match 8.5%; Score 220; DB 1; Length 416;
 Best Local Similarity 23.3%; Pred. No. 2,9e-07;
 Matches 116; Conservative 46; Mismatches 168; Indels 168; Gaps 25;
 Db 5 VRLALLL-----PAG-----PTWGSKEK-----CLTKMYT---TSGCCCKACNIG 42
 Qy 6 VPGLLPLVLPALLADVYVAGVGLVPHRGDLEKRESPCPOGKYNHNPONSTICCTCKHKG 65
 Db 6 VRLALLL-----PAG-----PTWGSKEK-----CLTKMYT---TSGCCCKACNIG 42
 Qy 66 TVLVNDCPGRGRTDRCVAPG-TYALLENHRLRCLSCSRCDENQVSLPCVYNDRTV 124
 Db 43 EGVAVPC--GVNQTVCPCIDSVTVYEDVYATERPCKPCCTQCVG--LHSMAPCVESDDAV 98
 Qy 125 CGGRKNQYREYMETGPRCLNGLCPNG-TVINPCOBROPTIC-HCHMGFLKAGK---- 178
 Db 99 CRC---AYGYFOELSSCKECSICEVGRFLMPCDSDQTVCEBPEGFSDEANFVVP 155
 Qy 179 CLSCHDCK-----NKRCEKLCF-----TRPSTKDSQDPGT-----T 210
 Db 156 CLPCTICEBENWVWKECTATSDAECRDLHPRMTTHPSLAGSDSPPIITRDPENTGMAAT 215
 Qy 211 VILPLVVFGLCLASFASVVLACHRYQRKRLKYSITCGOSTLYKEBPELVAPRPNPT 270
 Db 216 TLADIYV-----TWGSSQPVVSRGTADNLIV----- 243
 Qy 271 TTICFSSPSSPSVPIPYI-----SCDRNFGAVALPSESTAPP-----HLKAGPIIP 319
 Db 244 ----YCSILAAVVGVAIYAFKRNKSCKNQGANRPNVQNPSPBGEKLIHSDGISVD 299
 Qy 320 GPAPASTHLCTPGPAPASTHLCTPGPAPASTHLCTPVQKWEASAFAPQDLADADPATIYAVV 379

Db 300 ----SQSLHDQCPPNQS---TQGP-----APKGDGSLYA-- 326
 Qy 380 DGVPSPR-----WKELVRLGLSEHERLEBLNGLHLAEAGYSMLAAR 424
 Db 327 -SLPSPKQEVERKLLSSSAEETWRQLAGELGYKEDLIDCFTR-----ESPALLADN- 379
 Qy 425 RRTPRRATLELLGRVLR 442
 Db 380 --SAKETATDALLVALR 395
 RESULT 14
 TRIB HUMAN
 ID TRIB HUMAN STANDARD; PRT; 461 AA.
 AC P20333; 016042; O9UINH;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept) [Contains: Tumor necrosis factor binding protein 2 (TBPII)].
 GN TNFRSF1B OR TNFR2 OR TNFR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_Taxid=9606;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=90260639; PubMed=2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;
 RA "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins";
 RL Science 248:1019-1023(1990).
 [2]
 SEQUENCE FROM N.A. AND VARIANT ARG-196.
 RX MEDLINE=91045991; PubMed=2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RA "A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 [3]
 SEQUENCE FROM N.A.
 RX MEDLINE=96299745; PubMed=8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepailler D., Stallard B.J., Goeddel D.V., Desautave F.J.;
 RA Brodeur G.M.;
 RL "Physical mapping and genomic structure of the human TNFR2 gene";
 RL Genomics 35:94-100(1996).
 [4]
 SEQUENCE OF 37-461 FROM N.A.
 RX MEDLINE=91370690; PubMed=1966549;
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R., Brockhaus M., Leeseleuer W.;
 RL "Two human TNF receptors have similar extracellular, but distinct intracellular, domain sequences";
 RL Cytokine 2:231-237(1990).
 [5]
 SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
 RX MEDLINE=90349572; PubMed=2166946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;
 RL "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
 [6]
 SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
 RX MEDLINE=21069356; PubMed=11197692;
 RA Tauchiya N., Komatsu T., Matsushita M., Ohashi J., Tokunaga K.;
 RL "New single nucleotide polymorphisms in the coding region of human TNFR2: association with systemic lupus erythematosus";
 RL Genes Immun. 1:501-503(2000).

RN [7]
 RP SEQUENCE OF 27-31.
 RX MEDLINE=90110215; PubMed=2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 urine. Evidence for immunological cross-reactivity with cell surface
 tumor necrosis factor receptors";
 RL J. Biol. Chem. 265:1531-1536(1990).
 RN [8]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE=91056048; PubMed=2173696;
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Bruckhaus M.;
 RT "Purification and partial amino acid sequence analysis of two
 distinct tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [9]
 RP CHARACTERIZATION.
 RX MEDLINE=91016040; PubMed=1328224;
 RA Penhica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 Characterization of ligand binding, internalization, and receptor
 phosphorylation";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [10]
 RP INTERACTION WITH TRAF2.
 RX MEDLINE=94349371; PubMed=8069916;
 RA Roche M., Wong S.C., Henzel W.J., Goeddel D.V.;
 RT "A novel family of putative signal transducers associated with the
 cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
 RL Cell 78:681-692(1994).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
 TRAF2.
 RX MEDLINE=99221490; PubMed=10206649;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RT "Structural basis for self-association and receptor recognition of
 human TRAF2.";
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
 approximately 5-fold lower affinity for homotrimeric
 TNFSF1/lymphotxin-alpha. The TRAF1/TRAF2 complex recruits the
 apoptotic suppressors BIRC2 and BIRC3 to TNFSF1B/TNFR2.
 CC -1- SUBUNIT: Binds to TRAF2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
 CC -1- PTM: Phosphorylated; mainly on serine residues and with a very low
 level on threonine residues.
 CC -1- PTM: A soluble form (tumor necrosis factor binding protein 2) is
 produced from the membrane form by proteolytic processing.
 CC -1- PHARMACEUTICAL: Available under the name Embrel (Immunex and
 Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
 arthritis (RA). Embrel consist of the extracellular ligand-binding
 portion of TNFR1 linked to an immunoglobulin Fc chain. It binds to
 TNF-alpha and blocks its interactions with receptors.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD120b entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm";
 CC -1- DATABASE: NAME=Embrel; NOTE=Clinical information on Embrel;
 WWW="http://www.embrel.com/";
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M3215; AAC59929.1; -;
 DR EMBL; U52165; AAC50622.1; -;
 DR EMBL; U52156; AAC50622.1; JOINED.
 DR EMBL; U52157; AAC50622.1; JOINED.

DR EMBL; U52158; AAC50622.1; JOINED.
 DR EMBL; U52159; AAC50622.1; JOINED.
 DR EMBL; U52160; AAC50622.1; JOINED.
 DR EMBL; U52161; AAC50622.1; JOINED.
 DR EMBL; U52162; AAC50622.1; JOINED.
 DR EMBL; U52163; AAC50622.1; JOINED.
 DR EMBL; U52164; AAC50622.1; JOINED.
 DR EMBL; M55994; AAC36755.1; -;
 DR EMBL; S63368; AAB19824.2; -;
 DR EMBL; M35857; AAB63262.1; -;
 DR EMBL; AB030950; BAA89053.1; -;
 DR PIR; A35356; A35356.
 DR PDB; 1CA9; 12-APR-99.
 DR GeneW; HGNC:11917; TNFRSF1B.
 DR MIM; 191191; -;
 DR GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR_4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Phosphorylation; Pharmaceutical; Polymorphism; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 461
 FT FT
 FT CHAIN 27 461
 FT FT
 FT CHAIN 27 461
 FT FT
 FT DOMAIN 23 257
 FT TRANSMEM 258 287
 FT DOMAIN 288 461
 FT FT
 FT REPEAT 39 76
 FT REPEAT 77 118
 FT REPEAT 119 162
 FT REPEAT 163 201
 FT DISULFID 40 53
 FT DISULFID 54 67
 FT DISULFID 57 75
 FT DISULFID 78 93
 FT DISULFID 96 110
 FT DISULFID 100 118
 FT DISULFID 120 126
 FT DISULFID 134 143
 FT DISULFID 137 161
 FT DISULFID 164 179
 FT CARBOHYD 171 171
 FT CARBOHYD 193 193
 FT VARIANT 196 196
 FT FT
 FT VARIANT 232 232
 FT FT
 FT CONFLICT 141 141
 FT CONFLICT 363 363
 FT SEQUENCE 461 AA; 48291 MW; 603D0AE1CD65ACEF CRC64;
 SO
 Query Match 7.6%; Score 199; DB 1; Length 461;
 Best Local Similarity 25.3%; Pred. No. 7e-06;
 Matches 77; Conservative 26; Mismatches 103; Indels 98; Gaps 14;
 QY 32 PHRDLEKRESPPCGKYNHPONSTICCTCKCHKTYIYNDCPGGRDTDCRVCAPGTYTA 91
 DB 34 PEPG-----STGLREY-YDOTAKMCKSCSPQAHKVFCTKTS-DIVDCSCDSTYQ 85
 QY 92 LENTLRRLCLSC-SRCRDMEFVEISPCVVRDVTGCGRKNQYREYMGETGRCLNCSIC- 149
 DB 86 LMMVPECLSGSGSCSD--QVETQACTREONRICTRPGWCYALSKQDG-----CRICA 138
 QY 150 -----ENGTVINPCQERODPTICHCHMGFPLGKAKCISCHDCKNKECEKLCPTRPSTGKD 203
 DB 139 PLKRCRPGFVARPGTETSDVVC-----KPCA----- 165
 QY 204 SODPGTVLPLPLVVFGLCLASFASVYLACRYORMKRLIITIGGSTLYKEGSPBLVLP 263
 DB 166 ---PGT-----FSNTTSTYDICKPHQ-----ICN-----VVA 189

OY 264 ARGNPITTCSSSPSSS----PVSIPIYICSDNSNGAVASPSSETPAPHLKGPILP 319
 DB 190 IPGNASMAVCTISPTSRMAPGAVHLPQVSTRSGCHTPPEPS--TAPSTSFLLMGP 247
 OY 320 GPPA 323
 DB 248 GPPA 251

RESULT 15
 TR23_MOUSE STANDARD; PRT; 176 AA.
 AC Q9ER63; OSVHC0; Rel. 41. Created
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB).
 GN TNFRSF23 OR TNFRSF1A1 OR TNFRH1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV; TISSUE=Embryonic stem cells;
 RX MEDLINE=20519229; PubMed=11063728;
 RA Engemann S., Stredlicke M., Paulsen M., Franck O., Reinhardt R., Lane N., Reik W., Walter J.;
 RT "Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting."; Hum. Mol. Genet. 9:2691-2706(2000).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Pan G., Mao W., Ribber P.;
 RT "Characterization of SOB, a member of the TNFR family."; Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RL [3]
 RP SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ278264; CAC16405.1; -
 DR EMBL; AJ278505; CAC27352.1; -
 DR EMBL; AY046550; AAL05072.1; -
 DR HSSP; P19438; 1EXT.
 DR MGD; MGI:1930269; Tnf6f23.
 DR InterPro: IPR001368; Tnfr6f23.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
 FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 10 30 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).
 FT DOMAIN 31 176 EXTRACELLULAR (POTENTIAL).
 FT REPEAT 37 72 TNFR-CYS 1.
 FT REPEAT 74 114 TNFR-CYS 2.
 FT REPEAT 115 155 TNFR-CYS 3.
 FT DIDULFD 38 49 BY SIMILARITY.
 FT DIDULFD 50 63 BY SIMILARITY.
 FT DIDULFD 53 72 BY SIMILARITY.
 FT DIDULFD 75 90 BY SIMILARITY.
 FT DIDULFD 93 106 BY SIMILARITY.

FT DISULFD 96 114 BY SIMILARITY.
 FT DISULFD 116 131 BY SIMILARITY.
 FT DISULFD 134 147 BY SIMILARITY.
 FT DISULFD 137 155 BY SIMILARITY.
 FT CARBOHYD 148 148 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 176 AA; 19594 MW; EE30D617F49DB7D CRC64;

Query Match 7.5%; Score 196; DB 1; Length 176;
 Best Local Similarity 31.1%; Pred. No. 4e-06;
 Matches 51; Conservative 18; Mismatches 63; Indels 32; Gaps 8;

OY 9 LLLPLVLPALADYYPAGVQGLVPHPGDLEKRESPPQSGKYHPQNSTICTCKHKTLYL 68
 DB 18 LLLPLVLPVIFA-----MP-----ESYFNCPDGEY---QSNVCCCKTCPSGTFV 59
 OY 69 YNDCEGPERDTCRCVACPGITYALENHLRCLSCSRCDENFQVYISFCVVDRTVCGCR 128
 DB 60 KAPCKIPHTQCCCKCHGFTGTGKDNGLHDELCTCDKD--QNMVADCSATSDRKCEC- 116
 OY 129 KQYREYWGCTGF--RCINCSLCFNGTNTIP-----CQERDPTIC 166
 DB 117 --QGLVYVDKFPBSCRPCTKCPG--IPVLOECNSTANTVVC 155

Search completed: September 13, 2003, 07:04:40
 Job time : 18 secs

.Tue Sep 16 09:11:47 2003

US-09-970-532-2.rpt

Page 1

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 13, 2003, 07:01:54 ; Search time 39 Seconds

(without alignments)
3116.481 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603
Sequence: 1 MGLPTVGLLPLVLPALLA.....NIEALGASRLASEPRLW 471

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1589.5	61.1	446	6	Q95ND3
2	790	30.3	189	6	Q95185
3	776	29.8	189	6	Q97530
4	400.5	15.4	413	11	Q95MML
5	360	13.8	387	11	Q95MML
6	220.5	8.5	417	11	Q8VD70
7	220.5	8.5	427	11	Q8BYT1
8	211.5	8.1	368	13	Q8CFT3
9	210	8.1	368	13	Q8CFT3
10	206.5	7.9	387	13	Q91AR7
11	201.5	7.7	433	11	Q91ZM6
12	200	7.7	368	13	Q9PW79
13	199.5	7.7	651	13	Q98SM6
14	191	7.3	322	12	Q72761
15	187.5	7.2	302	13	Q9PUS0
16	187.5	7.2	357	13	Q9DF34

17	185.5	7.1	283	6	Q9XS28	Q9XS28 cercopithec
18	185	7.1	320	12	Q57079	Q57079 compox viru
19	180.5	6.9	401	13	Q9PRG7	Q9PRG7 xenopus lae
20	178	6.8	350	12	Q57123	Q57123 compox viru
21	177.5	6.8	267	6	Q02764	Q02764 oryctolagus
22	176	6.8	347	12	Q57119	Q57119 compox viru
23	176	6.8	351	12	Q57121	Q57121 compox viru
24	175	6.7	360	12	Q57118	Q57118 compox viru
25	174	6.7	316	12	Q57092	Q57092 ectromelia
26	174	6.7	317	13	Q8JFV6	Q8JFV6 brachydanio
27	174	6.7	320	12	Q57091	Q57091 ectromelia
28	174	6.7	320	12	Q57300	Q57300 ectromelia
29	173.5	6.7	289	11	Q8K2X6	Q8K2X6 mus musculu
30	173.5	6.7	347	12	Q57115	Q57115 compox viru
31	173	6.6	459	11	Q62327	Q62327 mus musculu
32	172	6.6	351	12	Q57117	Q57117 compox viru
33	172	6.6	438	13	Q9DFV0	Q9DFV0 brachydanio
34	169.5	6.5	349	12	Q57305	Q57305 compox viru
35	169	6.5	326	12	Q57122	Q57122 compox viru
36	168.5	6.5	482	11	Q88734	Q88734 mus musculu
37	165	6.3	457	4	Q81V86	Q81V86 homo sapien
38	164.5	6.3	349	12	Q57109	Q57109 variola vir
39	164	6.3	547	5	Q818Y2	Q818Y2 giardia lam
40	164	6.3	547	5	Q818V1	Q818V1 giardia lam
41	163.5	6.3	320	6	Q9XS29	Q9XS29 oryctolagus
42	163.5	6.3	348	12	Q57112	Q57112 variola vir
43	163.5	6.3	349	12	Q57111	Q57111 variola vir
44	163.5	6.3	349	12	Q57098	Q57098 camelpox vi
45	163.5	6.3	349	12	Q57284	Q57284 camelpox vi

ALIGNMENTS

RESULT 1
Q95ND3 PRELIMINARY; PRT; 446 AA.
ID Q95ND3
AC Q95ND3
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Tumor necrosis factor type I.
GN TNFR I.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxId=9685;
XM [1]
XP SEQUENCE FROM N.A.
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "Molecular cloning of feline tumor necrosis factor receptor type I
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in
RT cats.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051103; BAB55455.1;
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR006209; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS0186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00650; TNFR_NGFR_2; 3.
SQ SEQUENCE 446 AA; 49563 MW; 217BD331D08A74AA CRC64;

Query Match 61.1%; Score 1589.5; DB 6; Length 446;
Best Local Similarity 66.0%; Pred. No. 1e-125;
Matches 311; Conservative 39; Mismatches 94; Indels 27; Gaps 6;

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Oy 1 MGIPTAPGILLPLVLPALLADVYPAVOGIVHPHGBLEKRBSPCGKXKHPHONSTICT 60
Db 1 MGIPTAPGILLQPIVLALALVEIPLIVATGIVLPHLRERGRALPCPGKXIHODDUSICT 60
Oy 61 KCHKGTLYNDCEGPGHDTGRCVACGTYATALENHRLRCCLSCSRCDENFOYVISPVD 120
Db 61 KCHKGTLYNDCAAGPLDTCRECEMGSTFASENVLRQCLSCSKRKEMQYVISPCTVY 120
Oy 121 RDIVCGGRKQRYEYMGETGFRCLNLSLCPNGYVNIPOEBODTICHIMGFELGACICI 180
Db 121 RDIVCGGRKQRYRYMSETHFOCLNLSLCLNGVQISCRETNYCTCAGFFLGANCV 180
Oy 181 SCHDC-KKKECEKLCPTRPSTGKDSDPGTTVLLPLVIFYGLCLASFASVVLACRYOBYK 230
Db 181 SCVNCCKNKEBCTKLCVPIVETVADPDQDGGTVLLPLVIFYGLCVLSF-SIGLCKRYORX 230
Oy 240 PKLYSITCGOGLTYKGBEPLVLPAPGPNFTTICSSFTSSPWSIPYICSDMSNGA 290
Db 240 SKLFSIYCGKSTPTKEBEPPLATGFGFSIIPSPTRSPSPTRP-SPTFSPDANLRA 290
Oy 300 VASPSSTAPPHLKAGILPGRPASTHILCTPGPASTHILCTGCPASTHILCTPYOWEAS 350
Db 298 -ASVSRMAPIPYGAGPILSAAPSS-----PIS-----TPVQKEDS 330
Oy 360 APSAPDOLADAPATLYAADVGPSPSRKELVRLGLSHEHIERLELENGRHLREAYSM 410
Db 335 THTORPADADADATLYAADVGPSPSRKEXFVRLTSLSHEHIERLELELONGRCLREAYSM 390
Oy 420 LAAMRRTPRREATLEILGRVLRDMMLGLTENIEGALGAARLISEPRL 470
Db 395 LAAMRRTPRREATLEILGRVLRDMMDLGLCEIIEALCAPSLAPRL 445

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RESULT 2
095185
ID 095185 PRELIMINARY; PRT; 189 AA.
AC 095185;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Tumour necrosis factor receptor p60 (Fragment).
GN
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Duchie S., Nasir L., Eckersall P.D.;
RT "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
RT partial cds.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.
DR HSSP; P19438; EXPT.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SMO0208; TNFR; 3.
DR PROSITE; PS01866; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PSS0050; TNFR_NGFR_2; 3.
KM Receptor.
FT NON_TER 189 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE803D7DBE CRC64;

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	Query Match Similarity	30.3%; Score 790; DB 6;	Length 189;
	Best Local Similarity	73.1%; Pred. No. 2e-59;	
	Matches	136; Conservative	18; Mismatches 32; Indels 0; Gaps 0
Oy	1	MGLPTVPGLLPLVLIALADYPAAGVOGLVHPEDLEKRESPPCQGGKYHNFONSTICTT	60
		:::::	
Db	1	MGLPTVPGIOLPLALVELVEIPRVGLGVHLDRDKRALPCGQGKIHFODNSICTT	60

Qy	61	KCHKGTLYYNPCPGGRPTDCVCA	PGYTYALENHLRRLCSRCDEHFOYEI	SPCVVD	120
Db	61	KCHKGTLYYNPCGGGLDIDCKE	CECENGFTYASENLYRQCLSSCKKENYO	VEISPCYIA	120
Qy	121	RDYVGGCRKNQYREYWGEGTGR	FLCINCSLCPNCTVNI	PCQERODTICHCHGFFLKAKCI	180
Db	121	RDYVGGCRKNQYRYWSETHFO	CLINCSLCTNCTVOISCKETONTYCT	CHAGFFLRGNECV	180
Qy	181	SCHDCK	186		
Db	181	SCWVCK	186		

ID	PRELIMINARY;	PRT;	189 AA.
AC	097530.		
DT	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Tumor necrosis factor receptor p60 (Fragment).		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_Taxid=9615;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=21109092; PubMed=1182158;		
RA	Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthe S.,		
RA	Bennett D.;		
RT	"Cloning of canine IL-1ra, TNFR and TIMP-2.";		
RL	Vet Immunol Immunopathol. 78:207-214 (2001).		
DR	EMBL; AF013955; RAD01516.1; -.		
DR	HSSP; P19438; TNF.		
DR	InterPro; IPR006209; EGF_1like.		
DR	InterPro; IPR01368; TNFR_c6.		
DR	Pfam; PF00020; TNFR_c6; 3.		
DR	SMART; SMO0208; TNFR; 3.		
DR	PROSITE; PS01186; EGF_2; 1.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.		
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.		
KW	Receptor.		
FT	NON_TER	189	189
SEQ	SEQUENCE	189 AA;	5D3AD6A5676BEE99 CRC64;

Query Match	29.8%	Score	776;	DB	6;	Length	189;
Beat Local Similarity	73.1%	Pred. No.	1.4e-57;				
Matches	136;	Conservative	15;	Mismatches	35;	Indels	0;
Gaps	0						
Qy	1	MGLPTVPGLLLPVL	PALLADVYPAGVGGLVPHPDLEKRESPPCQGGKYNHPQNTICT	60			
Db	1	MGLPTVPGLLLPVL	YLLALILEIPIYSVALVPHPNRVRKRIILCPQGGKYNHPQDSICT	60			
Qy	61	KCHKSTLYNDCPGGRDPTDRCVAPGTYTLLENLRRCCLSCSRCDENFQYEISPCVUD	120				
Db	61	KCHKSTLYNDCPGGLTDCCRECGNGFTFASNNLRCCCLSSCKRKNQYIISPCYV	120				
Qy	121	RDYVGGCRKNQYREYAGETGFRCLNCSLCPNGTVNI	PCQERODTICHGMGEFLKGAKCI	180			
Db	121	RDYVGGCRKNQYRFYASETLFQCNNGCSCLNGTVQISCOEKONITICTGAGGFLEHBCV	180				
Qy	181	SCHDCK	186				
Db	181	SCVNCK	186				
RESULT	4						
Q99MM1							
ID	Q99MM1	PRELIMINARY;	PRT;	413	AA.		
AC	Q99MM1;						
DT	01-JUN-2001	(Tremblrel, 17, Created)					

Db 383 L 383

RESULT 6

ID Q8BY1 PRELIMINARY; PRT; 417 AA.

AC Q8BY1, 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Tumor necrosis factor receptor 16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; Tissue=Skin;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK037248; BAC29775.1; --
 SO SEQUENCE 417 AA; 44672 MW; CD0440E7E70A617 CRC64;

Query Match 8.5%; Score 220.5; DB 11; Length 417;

Best Local Similarity 23.1%; Pred. No. 2,3e-10;

Matches 106; Conservative 63; Mismatches 166; Indels 123; Gaps 26;

QY 44 CPOGKYNHPONSTICTCKCHKGTLYVNDGPGRGDTDCRVCAPO-TYTALENHLRCLSC 102
 DB 25 CSTGMVTH---SGECCACNLGEGVAQPC--GANQTVCEPCLDSVTFSDVASATEPCCKPC 79
 QY 103 SRCRDMEFQYBISPCVVDRTVCGCRKNQRYEMGTGFRCLNCSLCPNGT-VNI PCOER 161
 DB 80 TECIG--LQSMAPCVADDAVAVCRCSYGYOD--EETG-RCEACSVGVSGSLVFSQDK 134
 QY 162 ODTIC-HCHMGFFLKAK---CISCHDK-----NKECEKLCPT----- 197
 DB 135 QNTVCEBCEBEGYISDEANHVDPCLPCTVCEDETEROLRECTPMADAECEI-PGRWITRST 193
 QY 198 PSTGKD-----SQDPTVLLPLVIVFGCLASFASVLAACRYORWKPKLYITICGOSTL 252
 DB 194 PREGSDVTTPTGTGEPAPPPERDLI-----ASTV-----ADVTVTWSSSQPV 235
 QY 253 VKEGPELLVPAAPGNPTTTCFSSSPSSSPVSIPIYI-----SCDRNFGVAASPSSE 306
 DB 236 VTRGTADNLIPV-----YCSILAAVVGVAIYAFKRWNSCKONKQANSRPVNO 285
 QY 307 TAPP-----HLKAGPILPGPASTHLCTPGPASTHLCTPGPAA-----STHLCTPVQKW 356
 DB 266 TPPEBEGKLSHDSG--ISVDSOSLH-----DOGHTOTASGQALKDGNYLSLPLTKR 337
 QY 357 EASAPAPDQADADPATLVAVVDGVPSPRWKELVRRIGLS-EHEIERLELNGRHLEA 415
 DB 338 E-----EVEKLLNGD-----TWRIHLAGELGYOPEH-----IDSEFTHACP 372
 QY 416 QYSMLAAMRRRTPRREATLELGRVLRDMDLGGLENI 453
 DB 373 VRALLASWGAQD---SATLDLALALRRIORADIVESL 407

RESULT 7

ID Q8CFT3 PRELIMINARY; PRT; 427 AA.

AC Q8CFT3, 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Similar to nerve growth factor receptor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Eye;
 RA Strausberg R;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC038365; AA038365.1; --
 KW Receptor.
 SO SEQUENCE 427 AA; 45647 MW; 7AC73263F7B31436 CRC64;

Query Match 8.5%; Score 220.5; DB 11; Length 427;

Best Local Similarity 23.1%; Pred. No. 2.4e-10;

Matches 106; Conservative 63; Mismatches 166; Indels 123; Gaps 26;

QY 44 CPOGKYNHPONSTICTCKCHKGTLYVNDGPGRGDTDCRVCAPO-TYTALENHLRCLSC 102
 DB 35 CSTGMVTH---SGECCACNLGEGVAQPC--GANQTVCEPCLDSVTFSDVASATEPCCKPC 89
 QY 103 SRCRDMEFQYBISPCVVDRTVCGCRKNQRYEMGTGFRCLNCSLCPNGT-VNI PCOER 161
 DB 90 TECIG--LQSMAPCVADDAVAVCRCSYGYOD--EETG-RCEACSVGVSGSLVFSQDK 144
 QY 162 ODTIC-HCHMGFFLKAK---CISCHDK-----NKECEKLCPT----- 197
 DB 145 QNTVCEBCEBEGYISDEANHVDPCLPCTVCEDETEROLRECTPMADAECEI-PGRWITRST 203
 QY 198 PSTGKD-----SQDPTVLLPLVIVFGCLASFASVLAACRYORWKPKLYITICGOSTL 252
 DB 204 PREGSDVTTPTGTGEPAPPPERDLI-----ASTV-----ADVTVTWSSSQPV 245
 QY 253 VKEGPELLVPAAPGNPTTTCFSSSPSSSPVSIPIYI-----SCDRNFGVAASPSSE 306
 DB 246 VTRGTADNLIPV-----YCSILAAVVGVAIYAFKRWNSCKONKQANSRPVNO 295
 QY 307 TAPP-----HLKAGPILPGPASTHLCTPGPASTHLCTPGPAA-----STHLCTPVQKW 356
 DB 296 TPPEBEGKLSHDSG--ISVDSOSLH-----DOGHTOTASGQALKDGNYLSLPLTKR 347
 QY 357 EASAPAPDQADADPATLVAVVDGVPSPRWKELVRRIGLS-EHEIERLELNGRHLEA 415
 DB 348 E-----EVEKLLNGD-----TWRIHLAGELGYOPEH-----IDSEFTHACP 382
 QY 416 QYSMLAAMRRRTPRREATLELGRVLRDMDLGGLENI 453
 DB 383 VRALLASWGAQD---SATLDLALALRRIORADIVESL 417

RESULT 8

ID O57408 PRELIMINARY; PRT; 368 AA.

AC O57408, 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Subgroup B ALV receptor.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 NC NCB1_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97471016; PubMed=9326659;
 RA Adkins H.B., Brojatech J., Naughton J., Rolfs M.M., Resola J.M.,
 RA Young J.A.;
 RT "Identification of a cellular receptor for subgroup B avian leukosis
 RT virus".
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622(1997).
 DR EMBL; AF006002; AAB93987.1; --
 DR HSSP; 014763; 1D0G.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.

RT Expressed Xenopus Gene."
 RL Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF11890; AAD54072.1; -
 DR HSSP: P07174; INGR.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death_1.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR SMART: SM00005; DEATH_1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS50017; DEATH DOMAIN; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS50050; TNFR_NGFR_2; 4.
 DR Transmembrane.
 KW Transmembrane.
 SO SEQUENCE 387 AA; 42066 MW; 1A386A239C7C9A82 CRC64;

Query Match 7.9%; Score 206.5; DB 13; Length 387;
 Best Local Similarity 22.8%; Pred. No. 3,2e-09;
 Matches 101; Conservative 52; Mismatches 173; Indels 117; Gaps 23;

41 ESPPCGKYNHPQNSTICTCKCHKGYLYNDPCPGGRDTCRVCA-CTYALENHLRC 99
 Db EDVCSGLYT--NSGKCSLCPAGGVVPC--GSDTKCEPTIENSTFSDVRSKAKC 76
 100 LSCSRCDMEFOVEISPCVVDRTVCGCKKQRYREWGEGFRCLNCLCPNG-TVINPC 158
 Db OPCFTQSPSLTLE-SNCTREDTVCRPERQYLDNSG---ICLPQCLSKHGVSQC 131
 159 QERODTICH-CHMGPF--LKGAK--CISGH-DCKNKE-----C-----EKLCP-----T 196
 Db THNKNTVQCLCSGSEVKSSESPCLPCTECKEVEQIGCVQHDLMDKVPILK 191
 197 RPTGKSDPDPTVLLP-----LVIVFGCLASFAVYLAORYMKPKLYSIICGOS 250
 Db RTEGNGNSAGSPHPIPDNSKNIIPVY--CSILAAVVGILAYAF--KCYTCKCKK 247
 251 TLVKEPELVVAPGPNPTTICFSTSTSSSPVSIPIYISCDRSMFGVAAPSETAP 310
 Db QAKADAGELATSTGEKL-----HNSGVFLDTSLQEPN 283
 311 HLKAGPILPGPASTHLCTPGPASTHLCTPGPASTHLCTPVQKMEASAPAPDLADA 370
 Db HLSKATIEP-----KLYINLP--HNSQVERLADTSLGKD----- 318
 371 DPATLVAVVDGVPSPKMKELVRLGLSEHIERLELNGHLEAOYSMLAARRTPRR 430
 Db -----WQRLASLGYEERTIDTF---GRG-EDPVHTLTW---SSKE 354
 431 EATIELLGRVLRMDLGLCLEN 453
 Db SSTEVLCAALVNNRADVVENL 377

RESULT 11

Q912M6 PRELIMINARY; PRT; 433 AA.
 ID Q912M6
 AC Q912M6
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Tumor necrosis factor receptor type II (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Osburn B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.,
 RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
 RT capillary endothelial cells and participate in TNF-alpha transport
 RT through the blood-brain barrier."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF420214; AAL16021.1; -
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 KW Receptor.
 FT NON_TER
 FT NON_TER
 FT NON_TER
 FT NON_TER
 SO SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 7.7%; Score 201.5; DB 11; Length 433;
 Best Local Similarity 24.6%; Pred. No. 9,6e-09;
 Matches 84; Conservative 33; Mismatches 143; Indels 81; Gaps 16;

32 PHPDLEKRESPPGCKNHPQNSTICTCKCHKGYLYNDPCPGGRDTCRVCAPTTYA 91
 Db PEPG-----NOCQISQEVYDKKQMCCKCPGQYAKIPC-NKTSDTVCADCAAGMTQ 66
 92 LBNHLARCISC-SRCRDEMFOVEISPCVVDRTVCGCKKQRYREWGEGFRCLNCLCP 150
 Db VNNHLITCLSSSCSDD--QVETHNCTKQKNVCACNADSYCALKHSQ---NRCQW 120
 151 NGTVNIPQERODTICHCHMGFLKAKC---ISCHDCKNKECEYLCPRTSTGDSQD 206
 Db 121 K-----LSKCPGFGVARSRTSNGVICSAC-----APGTFSDTTS 156
 207 PGTVVLPVLYIVGCLASFAVYLAORYMKPKLYSIICGOSTLYKEGEPEL-----L 261
 Db 157 -STDVCRPHRICSLALPGNASTDVAVCSSPTPSAVP---RTIYSQEPFRSPMDQ 211
 262 VPAGFNPPTTICFSSPTSSSP-----VSIPYISCDRSMFGAV-----AS 302
 Db 212 EPGSQCPHPVPSIGSTPIIEPSTGSLPGLIVGLTTLGLMLGLANCFILVQRKK 271
 303 PS---SETAPHLKAGPILPGPAA---STHLCTPGPAPT 336
 Db 272 PSCLORETMVPHL---PDEKSQDAVGLDQOHLTLTAPSSS 309

RESULT 12

Q9PW79 PRELIMINARY; PRT; 368 AA.
 ID Q9PW79
 AC Q9PW79
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Tvrb3.
 DE TVB3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97100985; PubMed=8945512;
 RA Brojtatesch J., Naughton J., Rolfs M.M., Zingler K., Young J.A.;
 RT "CARL", a TNFR-related protein, is a cellular receptor for cytopathic
 RT avian leukosis-sarcoma viruses and mediates apoptosis."
 RL Cell 87:845-855(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brojtatesch J., Naughton J., Young J.A.T.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF161712; AAD47256.1; -
 DR HSSP: O14763; IDOG.
 DR InterPro: IPR001450; 4Fe4S_ferredoxin.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF000531; death_1.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00005; DEATH_1.

DR PÉam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
SQ SEQUENCE 322 AA; 35412 MW; 774549278D156A9D CRC64;

Query Match 7.3%; Score 191; DB 12; Length 322;

Best Local Similarity 31.4%; Pred. No. 5.3e-08;
Matches 49; Conservative 18; Mismatches 71; Indels 18; Gaps 7;

QY 27 VQGLVPHQDLEKRSPPCGKYNPNSTICTCKHKTYLYNDCPGGRDTCRCVAP 86
DB 18 VSGDVPY---EHNGKCKGTIDNSNN-LCKKQCDPGMYTHSC-NITSNKCAKCPD 71
QY 87 GTYALLENHLRRLSC-SRCDMEFQVEISPCVVDRTVCGCRKNQRYREYWGEGTGR-CL 144
DB 72 GTFTSIPNHIPTCLSGCRKCSN--QVETKSCNTQDRECVCAAGYCEFEBSNGCRLCV 129
QY 145 NCSLCPNGTVNIPCGERDPTIC-----HCHMGF 172
DB 130 PQTKCDSGYGVYGBSKGDVICKKCPGNIDKCMDF 165

RESULT 15

Q9PUS0 PRELIMINARY; PRT; 302 AA.

AC Q9PUS0;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAY-2003 (TRENBLREL. 23, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteocephalepterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2011091; PubMed=10642582;
RA Bobe J., Goetz P.W.;
RT "A tumor necrosis factor receptor homologue is up-regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation".
RL Biol. Reprod. 62:420-426(2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSSP; Q14763; 1D4V.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001368; TNFR_c6.
DR PÉam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR_2; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 7.2%; Score 187.5; DB 13; Length 302;

Best Local Similarity 28.7%; Pred. No. 9.7e-08;
Matches 52; Conservative 18; Mismatches 60; Indels 51; Gaps 10;

QY 56 TICTCTCHKTKTYLYNDCPGGRDTCRCVAPGTYALLENHLRRLSCSRCDMEFQVEIS 115
DB 33 SIYCDRCPPTTYRAPPSAM-RKSDCAECNPAVTEPMNHISKLCRSMCAEN--QVYKQ 89
QY 116 PCVVDRTVCGCRKNQY--REYWGEGTGRCLNCSLCPNG---TVNIPCGERDPTIC-HC 168
DB 90 ECSPSNKCECECEKGYFNKRYEA-----CIKHKECPGAGANTTGR---HQDTCEYQC 141
QY 169 HMGFP-----LKG-----AKTISCHDCKNKE-----CEKLCF 195
DB 142 QAGFYSEVSSAKATCLAQSNCKVGLRVVVKQDMHNTLCAACVLDLKTDRGAEYTHHILP 201
QY 196 T 196

DB 202 T 202

Search completed: September 13, 2003, 07:05:34
Job time : 42 secs